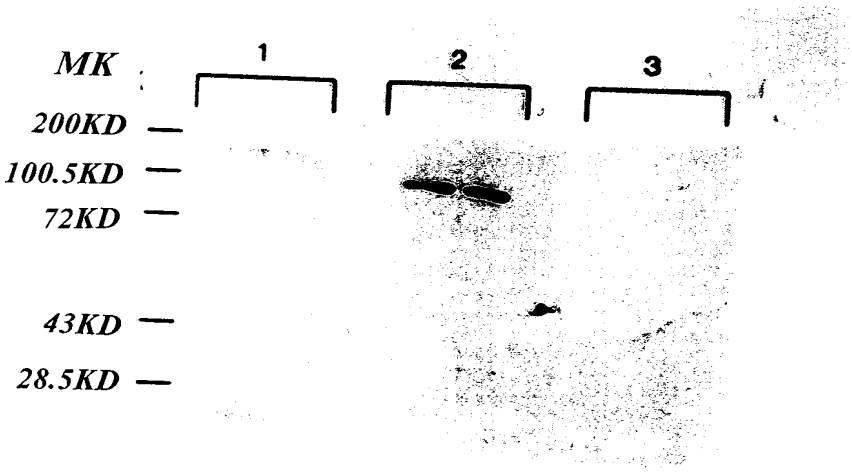
FIGURE 1



1 - anti- EGFr PoAB RK-2
2 - Cyt-356 MoAB/RAM
3 - RAM

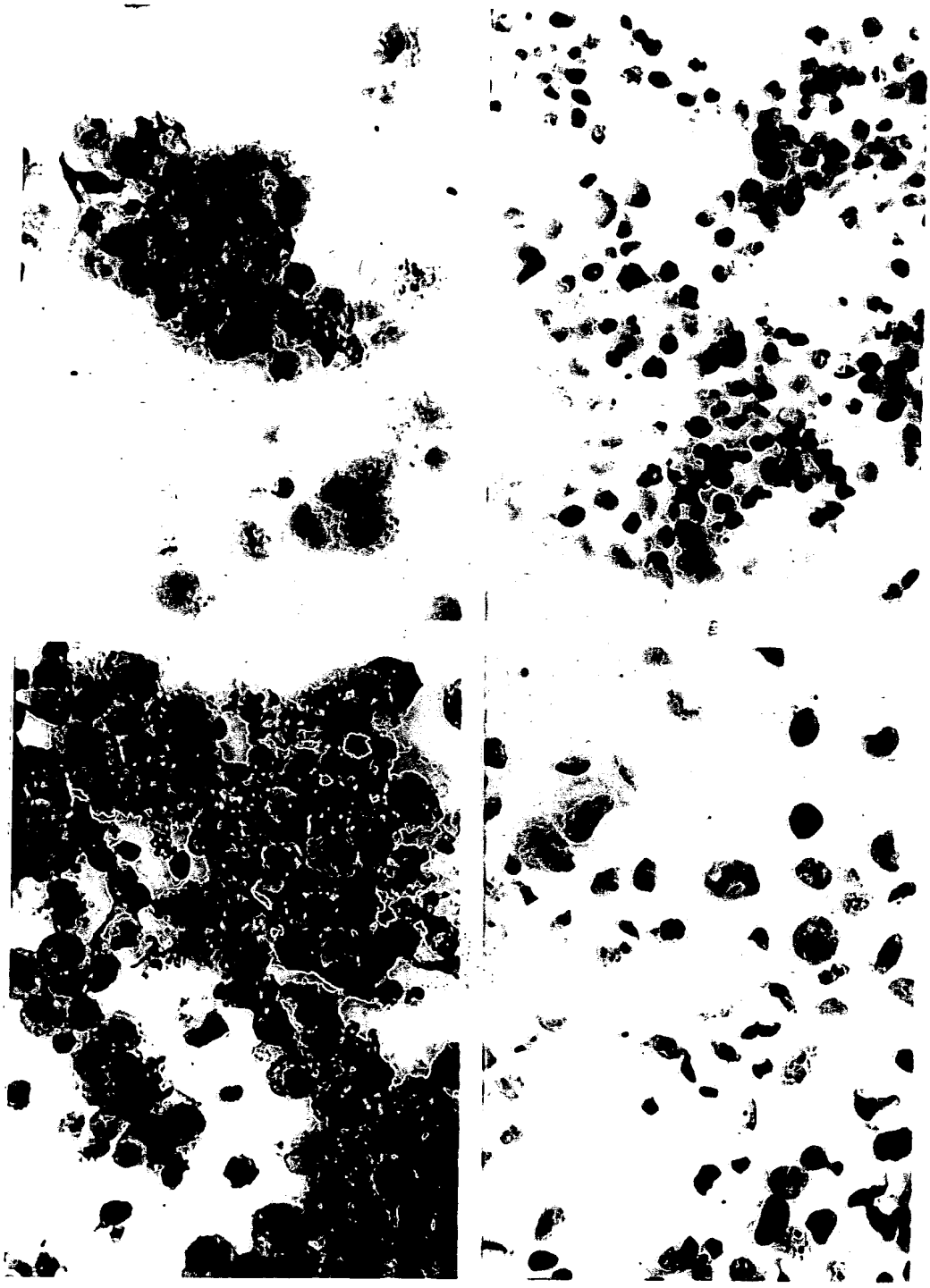


FIGURE 2B

FIGURE 2D

FIGURE 2A

FIGURE 2C

FIGURE 3B

FIGURE 3D

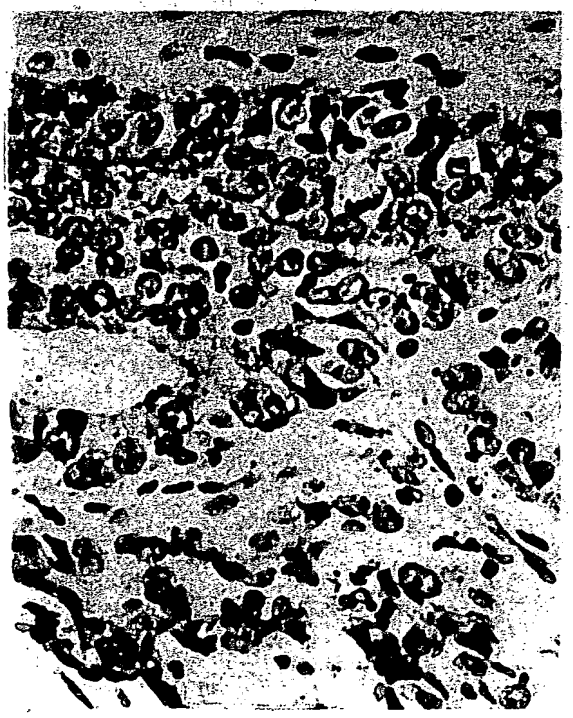


FIGURE 3A

FIGURE 3C

FIGURE 4

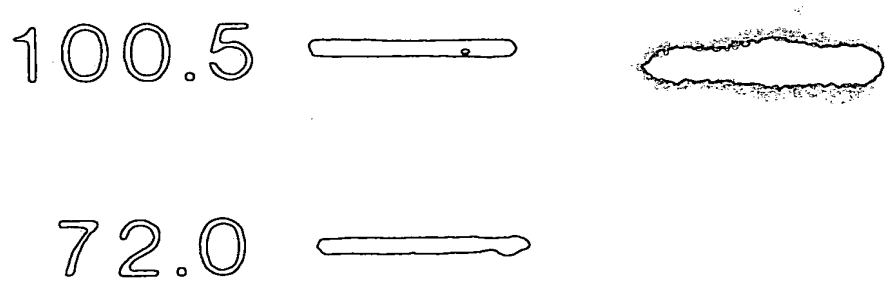


FIGURE 5

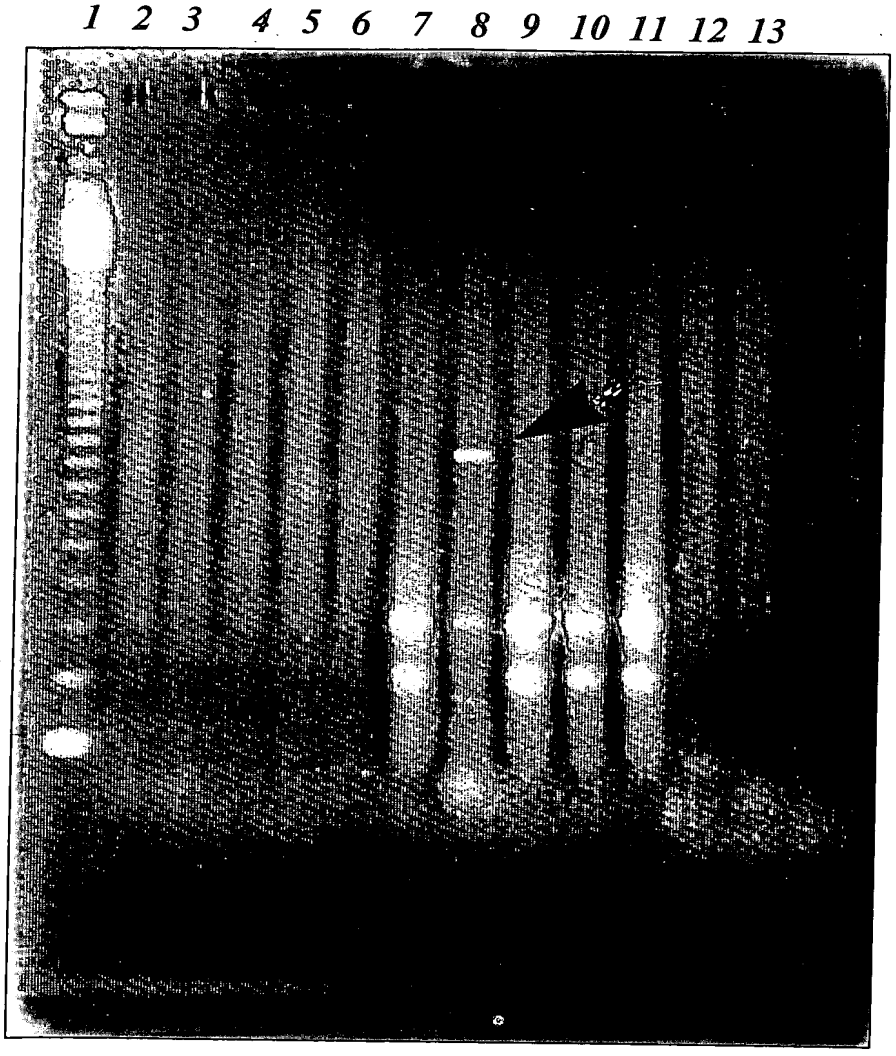


FIGURE 6A

FIGURE 6B

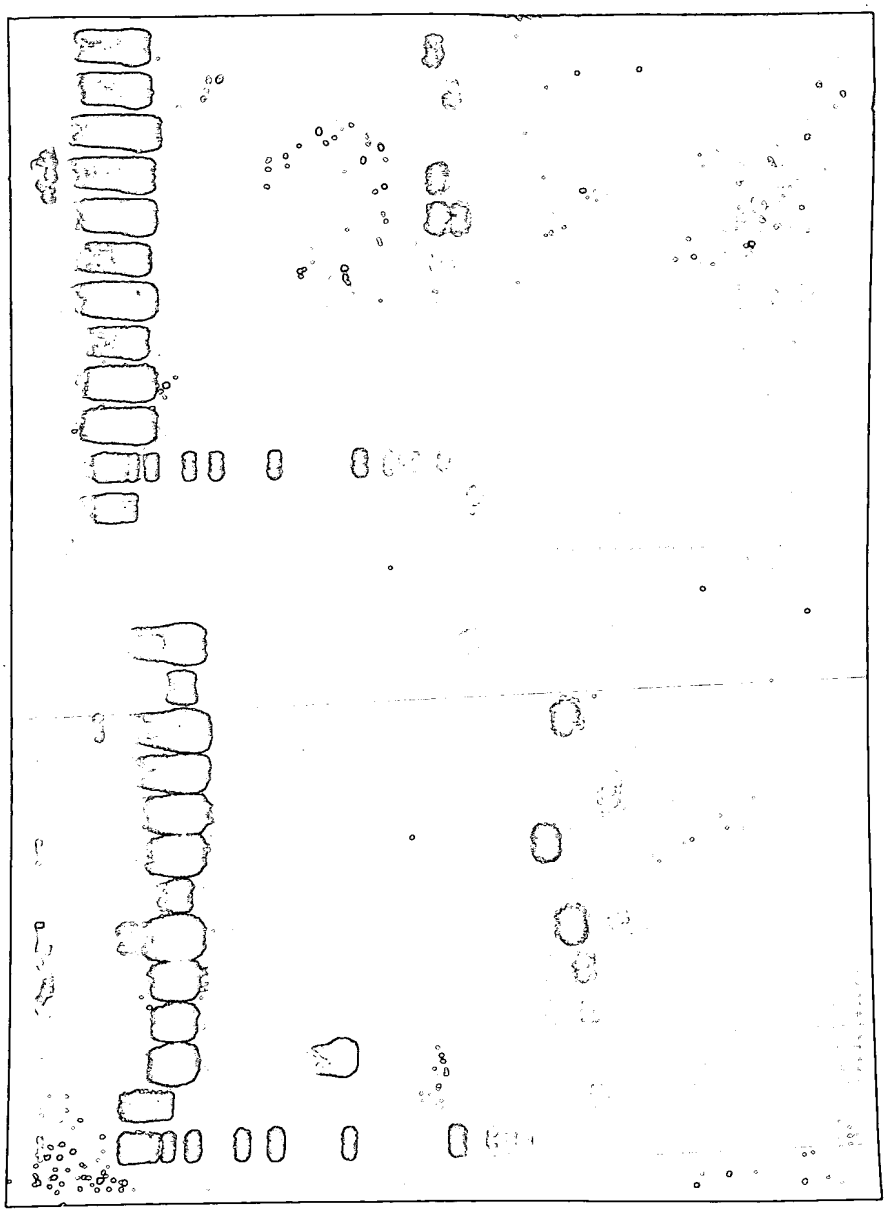


FIGURE 7

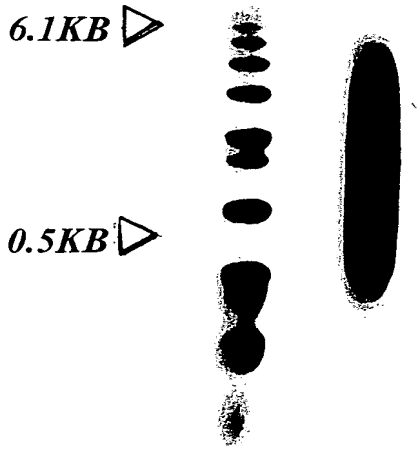


FIGURE 8

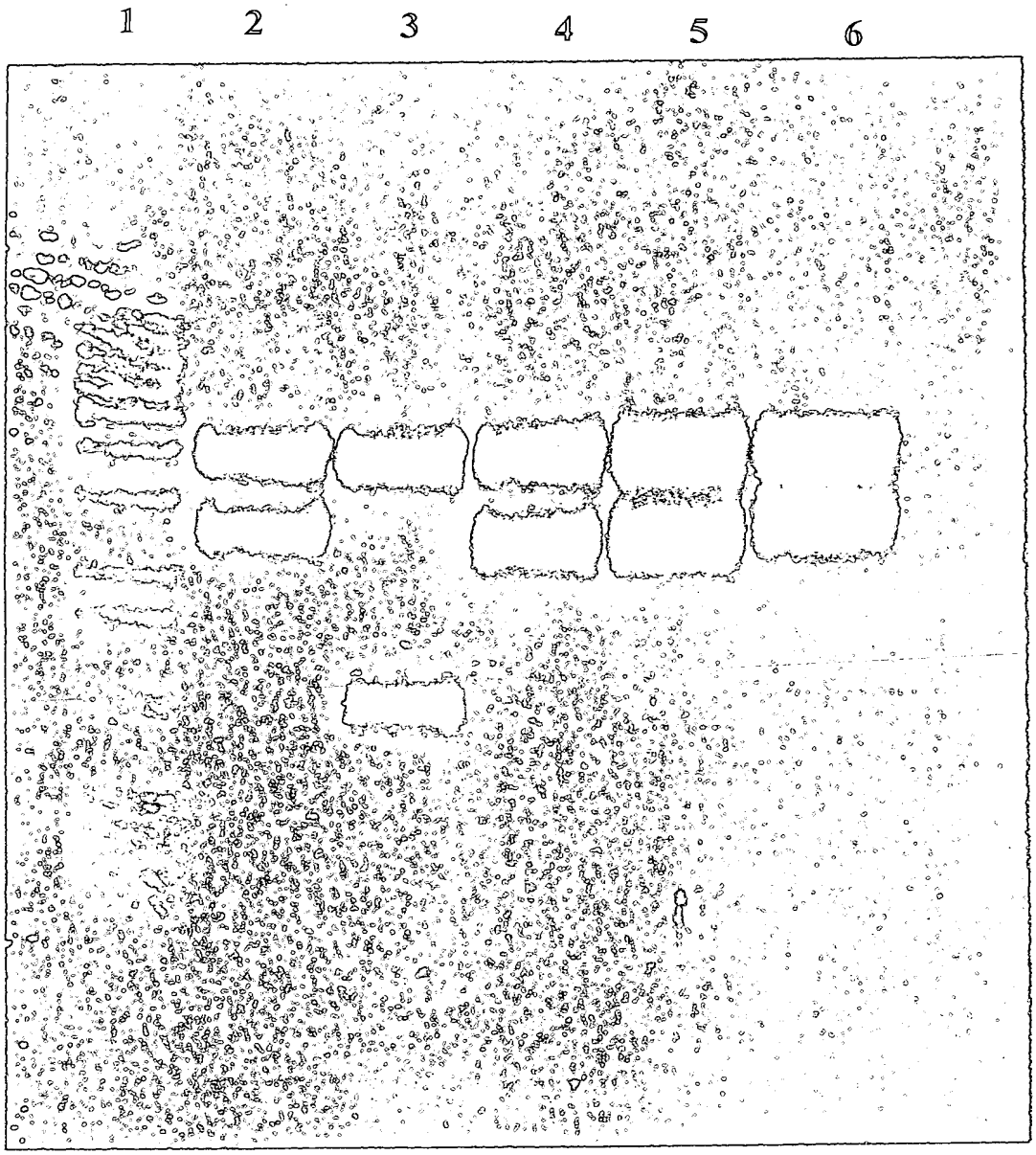


FIGURE 9

FIGURE 10

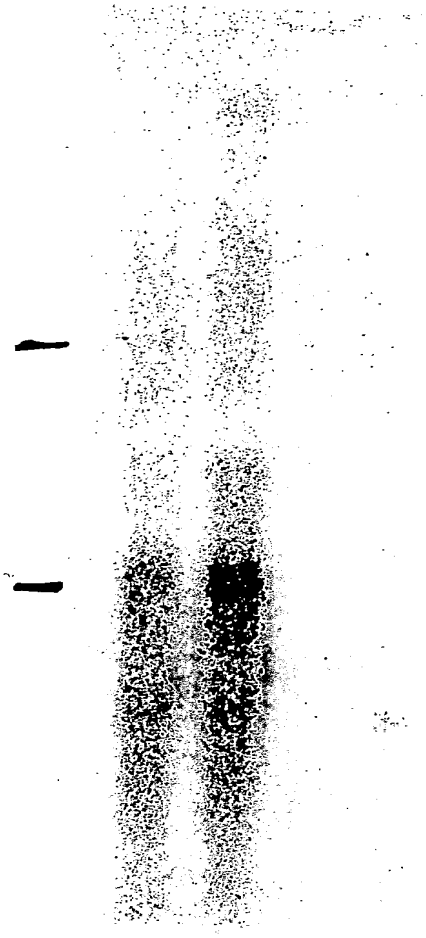
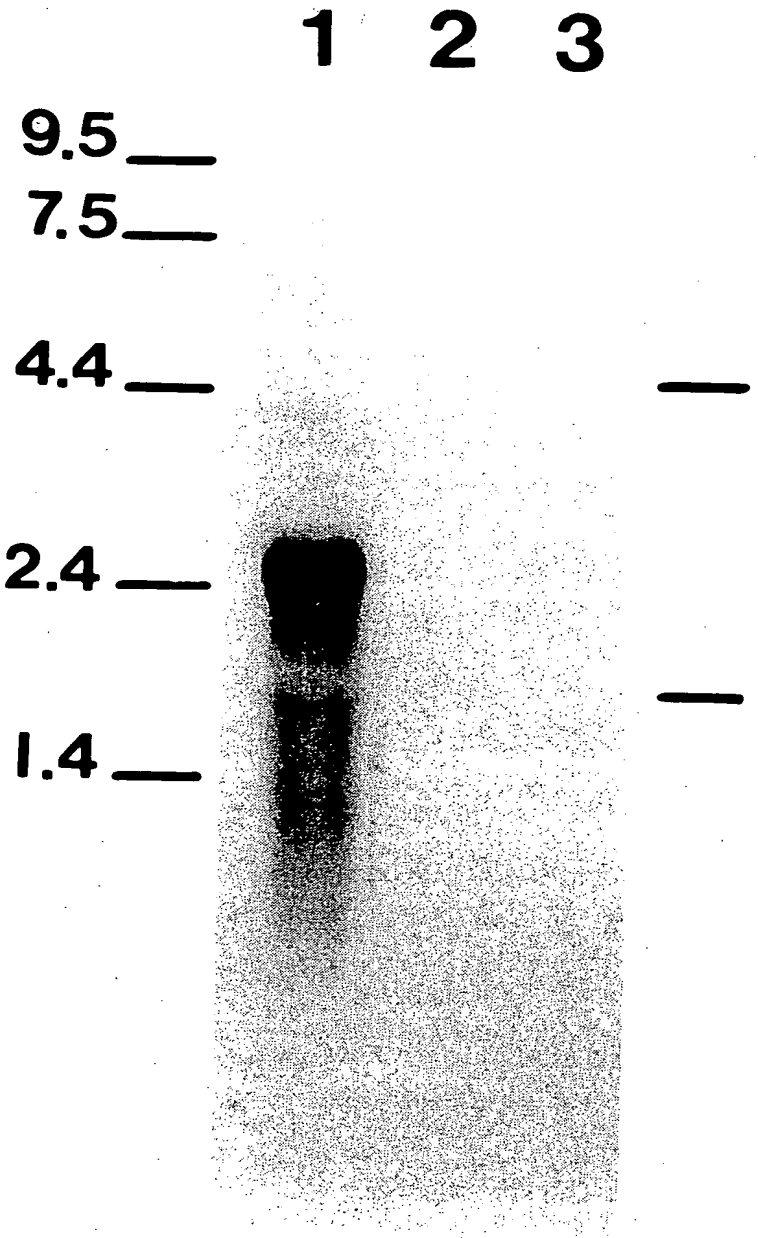


FIGURE 11



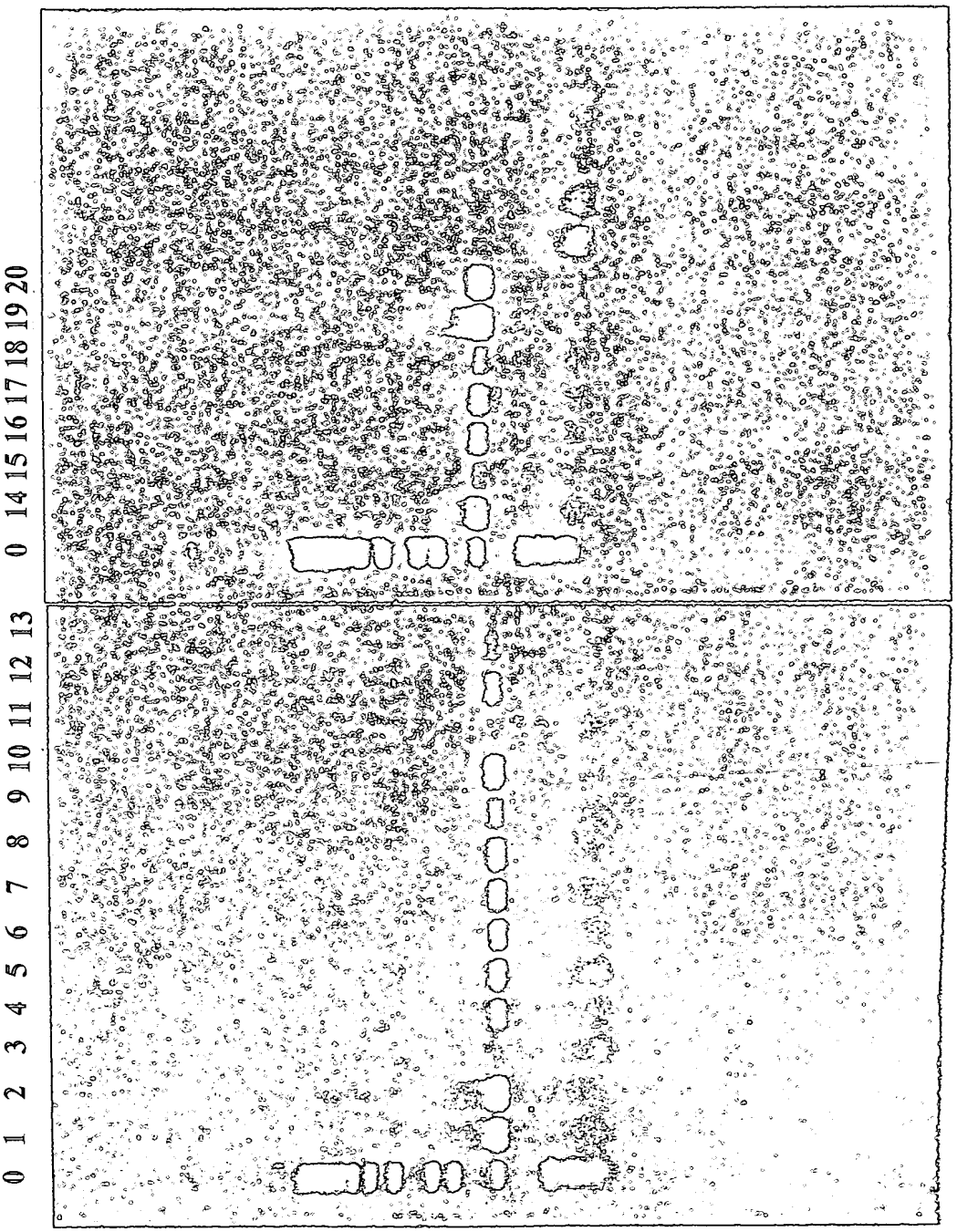


FIGURE 12A

FIGURE 12B

FIG. 13

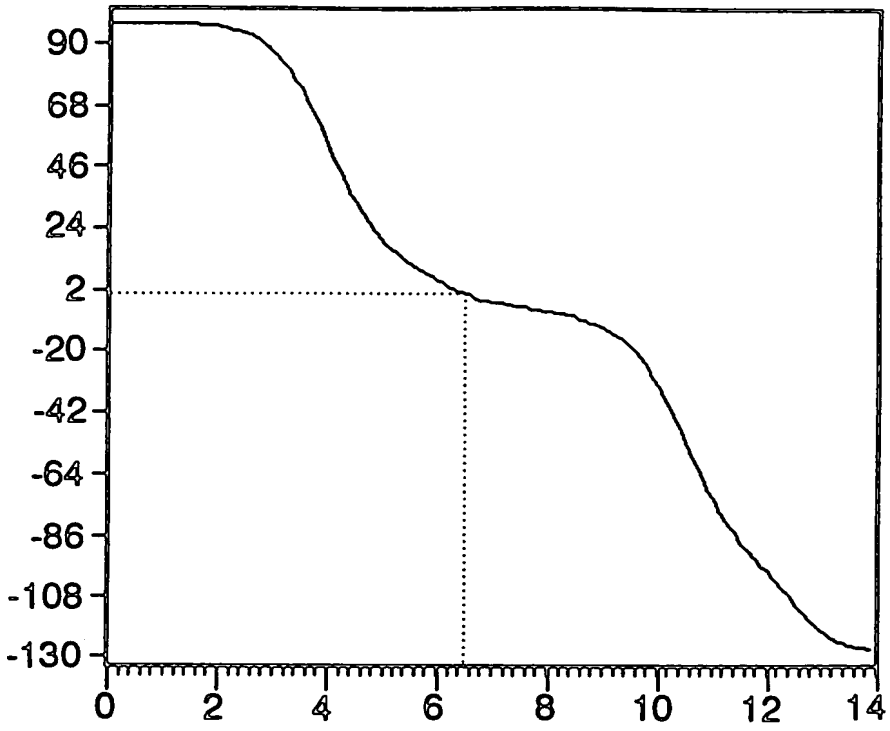


FIG. 14-1

Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

In Helical (H) conformation [DC = -75 CNAT] : 264 AA => 35.2%
In Extended (E) conformation [DC = -88 CNAT] : 309 AA => 41.2%
In Turn (T) conformation [DC = 0 CNAT] : 76 AA => 10.1%
In Coil (C) conformation [DC = 0 CNAT] : 101 AA => 13.4%

Sequence shown with conformation codes.
==========

Consecutive stretch of 5 or more residues in a given conformation are overlined.

1 H H H H H H H H H H H H H H E E E T T E E E E E E E E E E

31 E E E E E E H H H H H H C C C C C C T H H H H H H H H H H

61 H H H H H H H H H H H H E E E T T E E E E C C C C C H H H H

Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

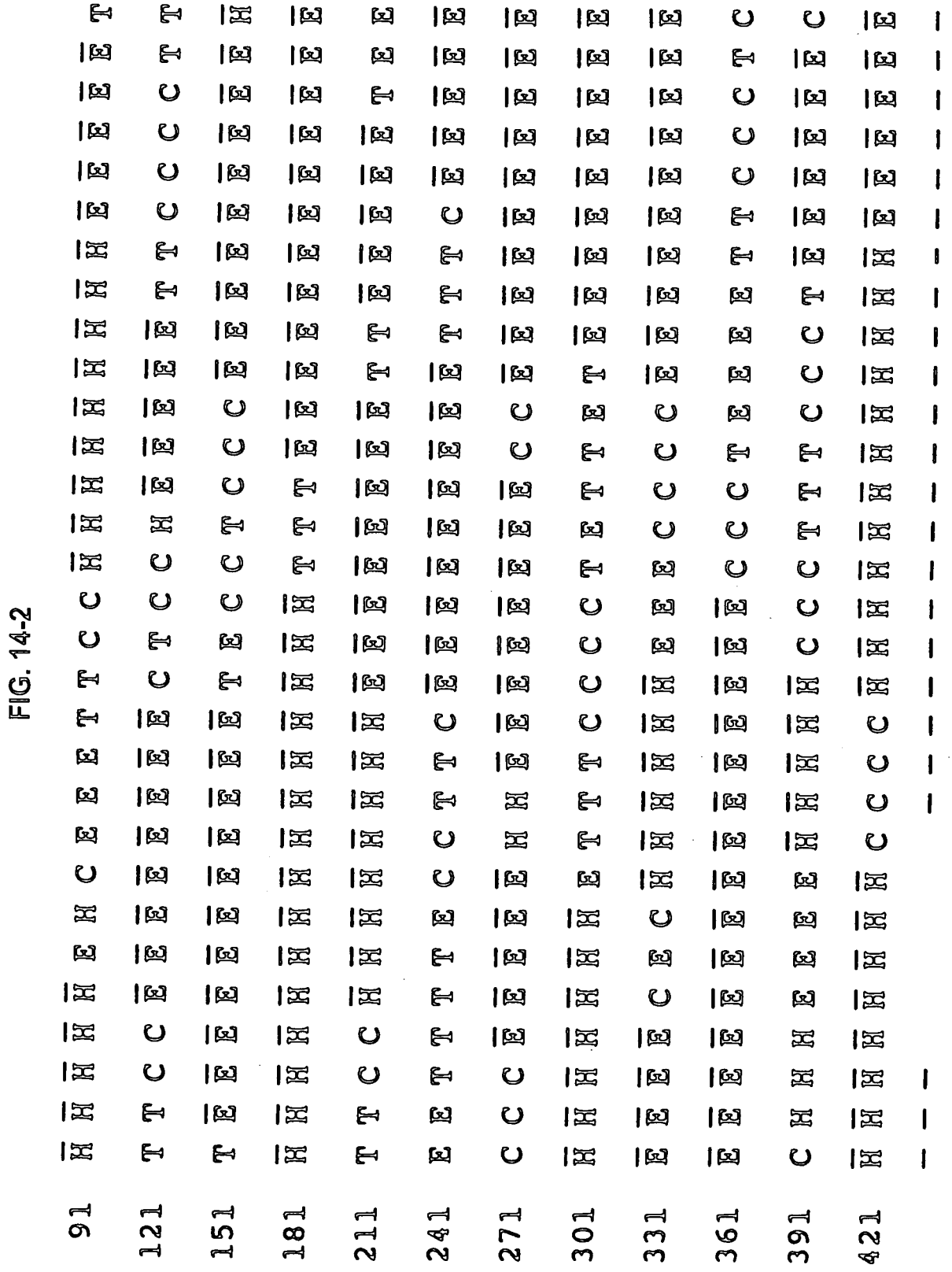


FIG. 14-2

FIG. 14-3

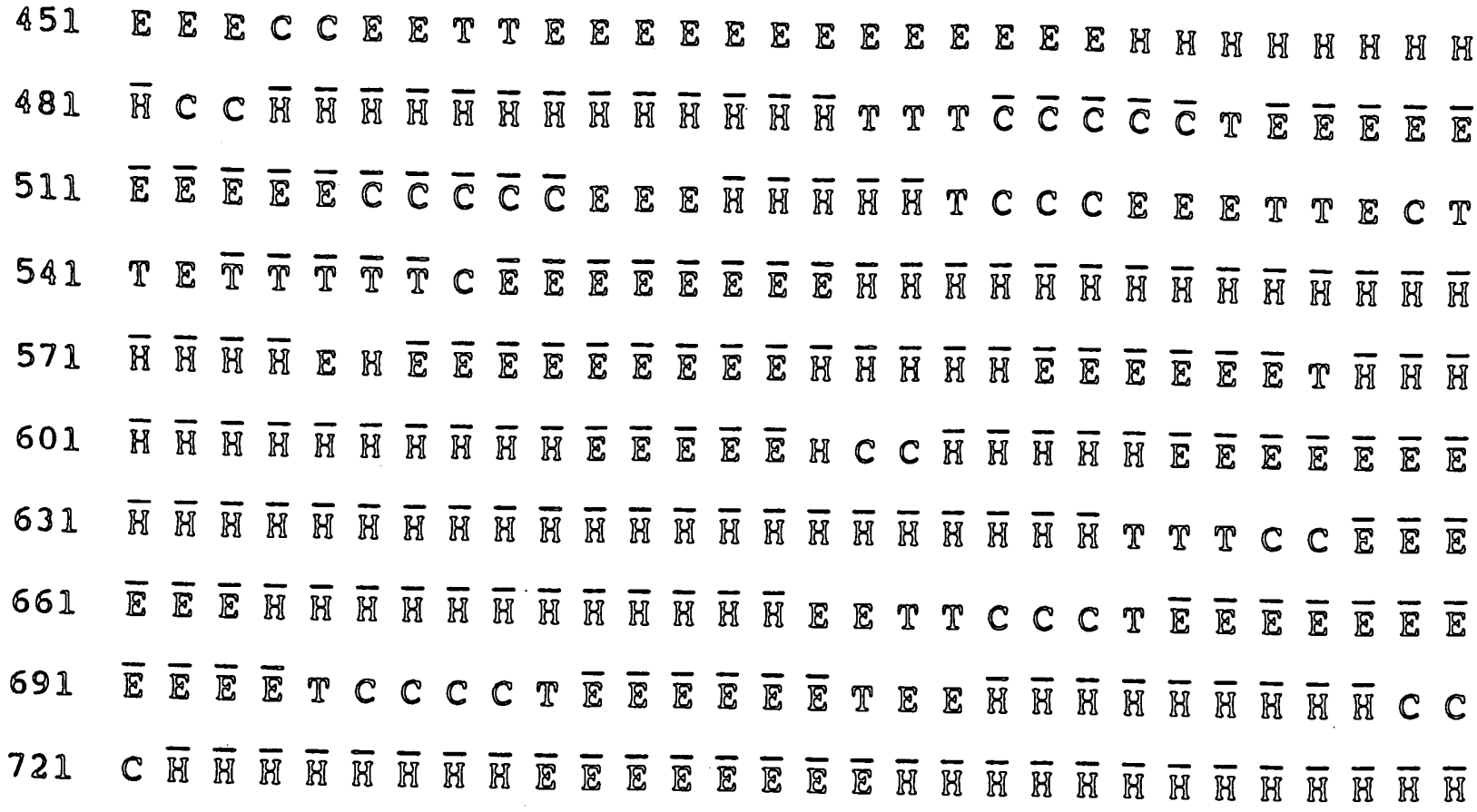
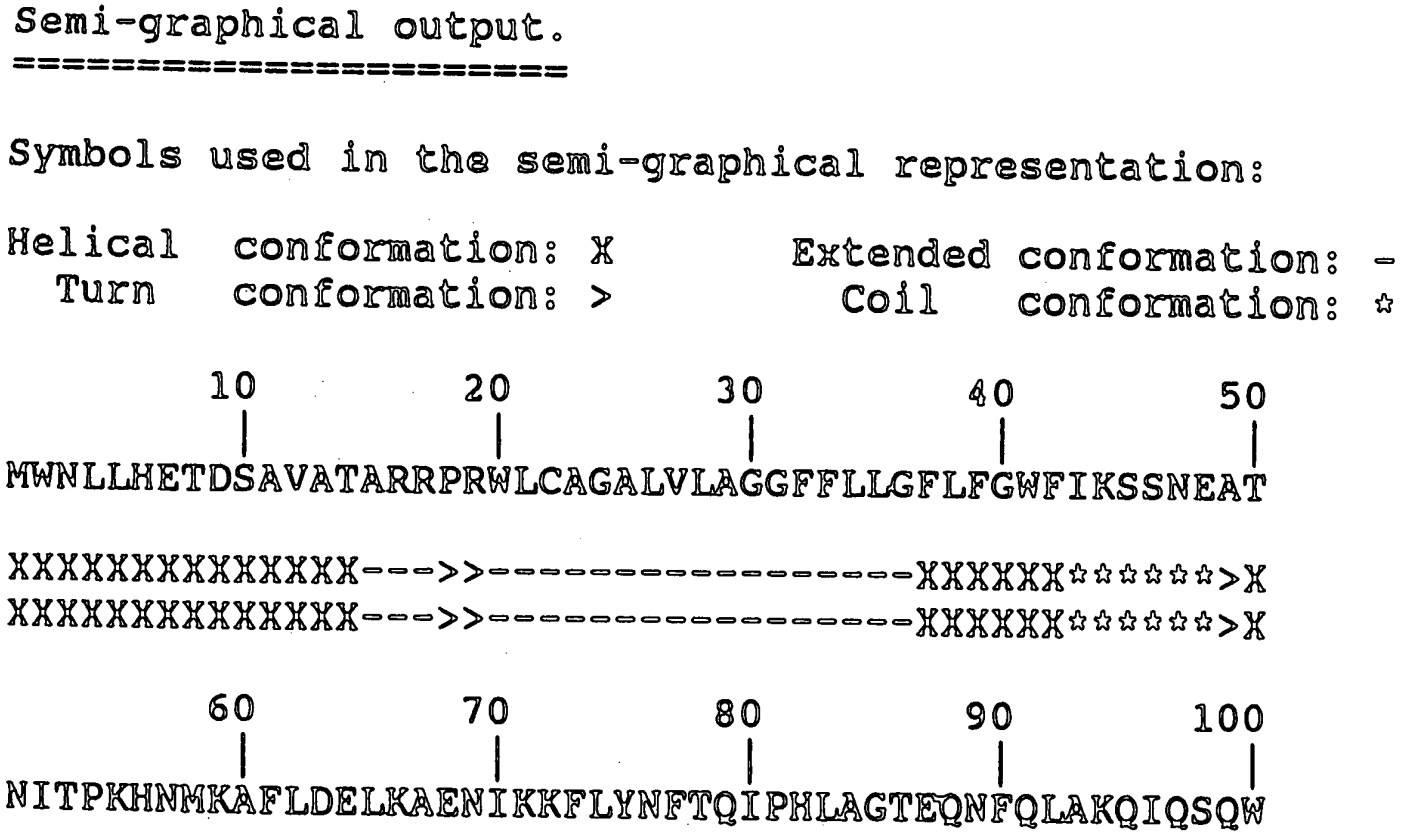

451 E E E C C E E T T E E E E E E E E E E E E H H H H H H H H
481 H C C H H H H H H H H H H H H H T T T C C C C C T E E E E E
511 E E E E E C C C C C E E E H H H H H T C C C E E E T T E C T
541 T E T T T T T C E E E E E E E E E H H H H H H H H H H H H H H
571 H H H H E H E E E E E E E E E H H H H H E E E E E E T H H H
601 H H H H H H H H H H E E E E E H C C H H H H H E E E E E E E E
631 H H H H H H H H H H H H H H H H H H H H H H H T T T C C E E E
661 E E E H H H H H H H H H H H H H E E T T C C C T E E E E E E E E
691 E E E E T C C C C T E E E E E E T E E H H H H H H H H H H C C
721 C H H H H H H H H H E E E E E E E E E H H H H H H H H H H H H H

FIG. 14-4



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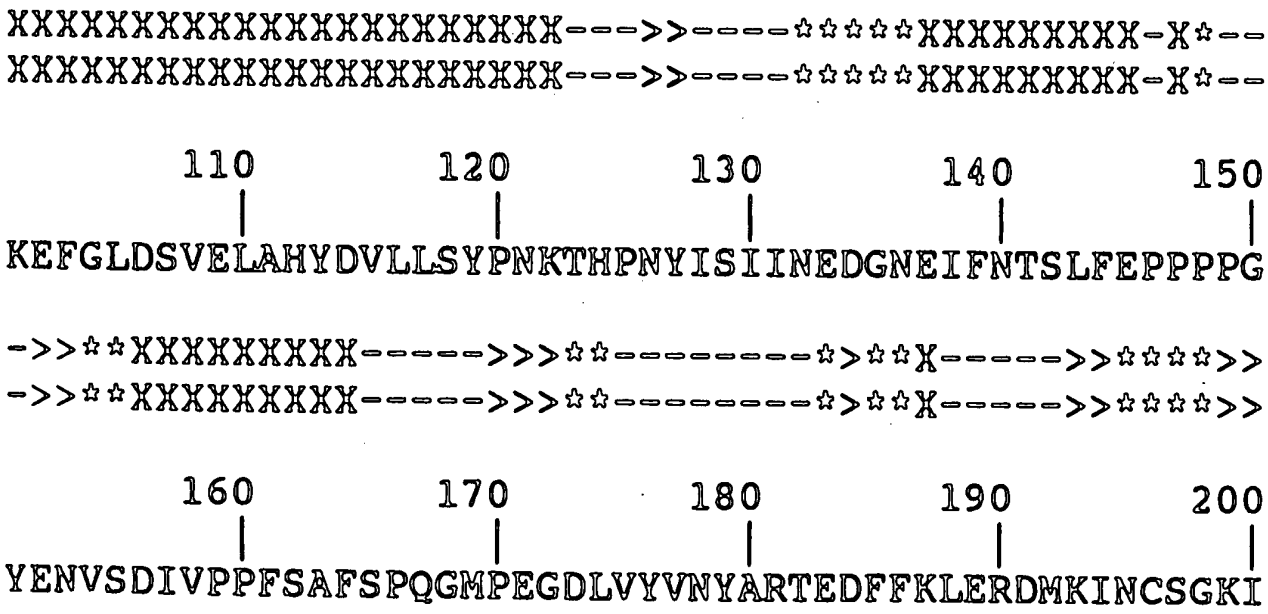
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 14-5



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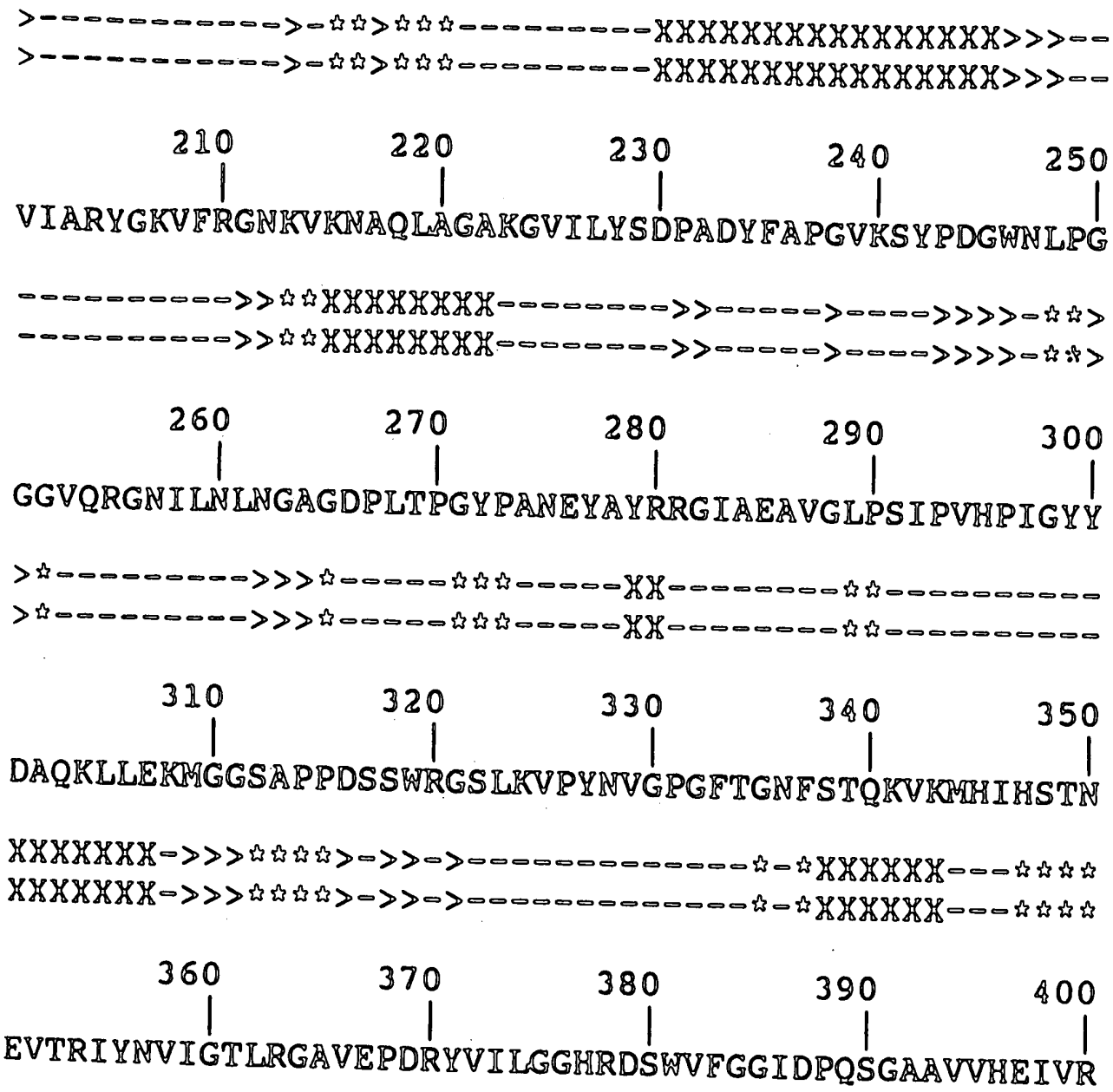
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 14-6



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Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 14-7

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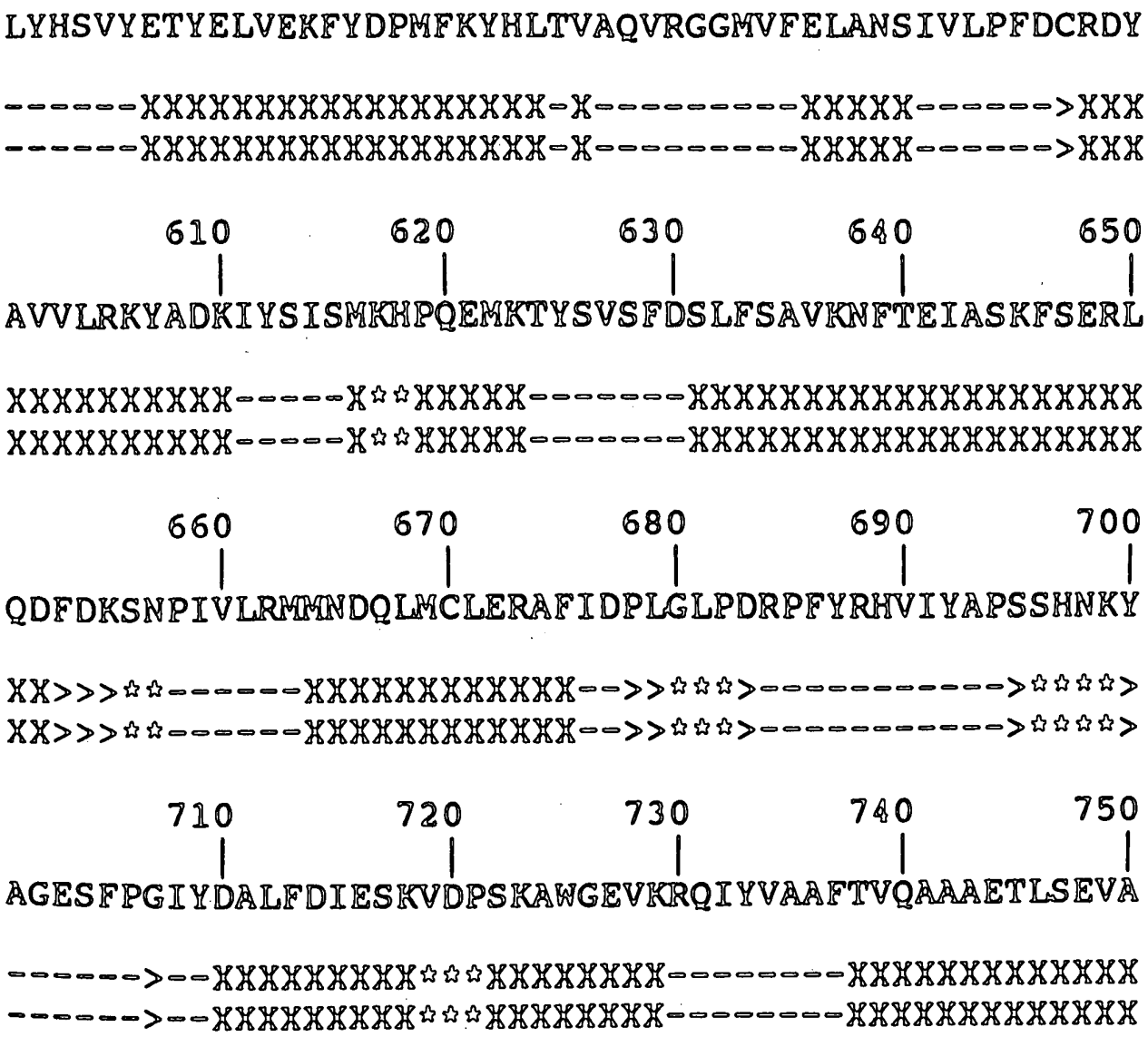
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 14-8



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Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 15A

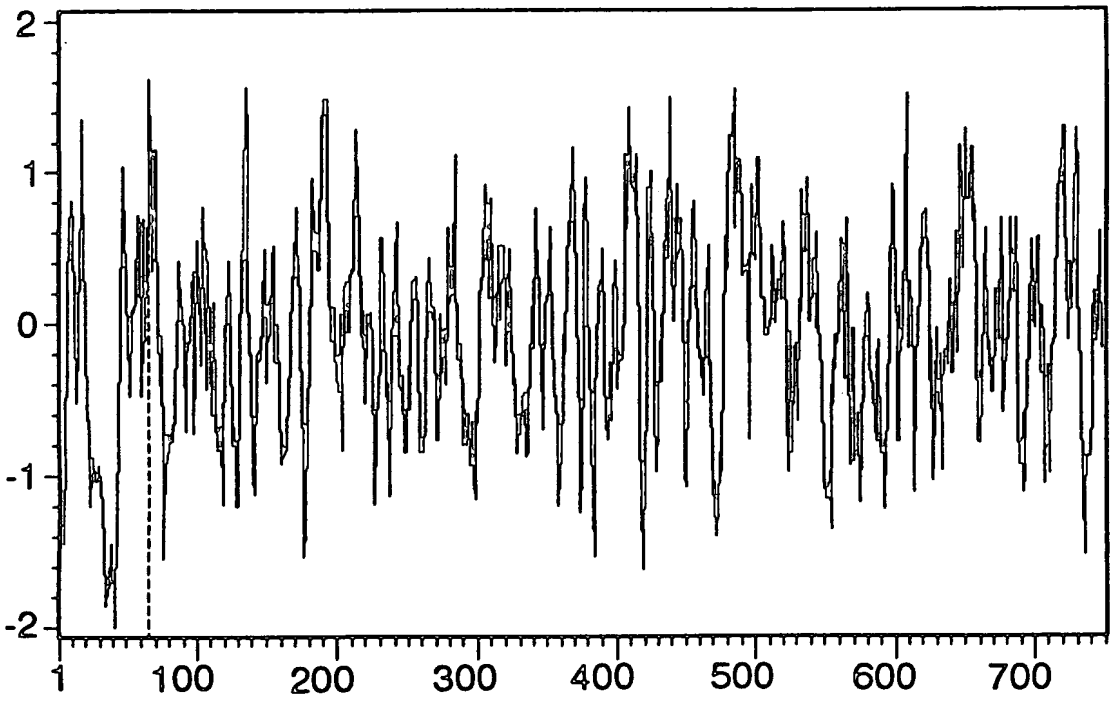


FIG. 15B

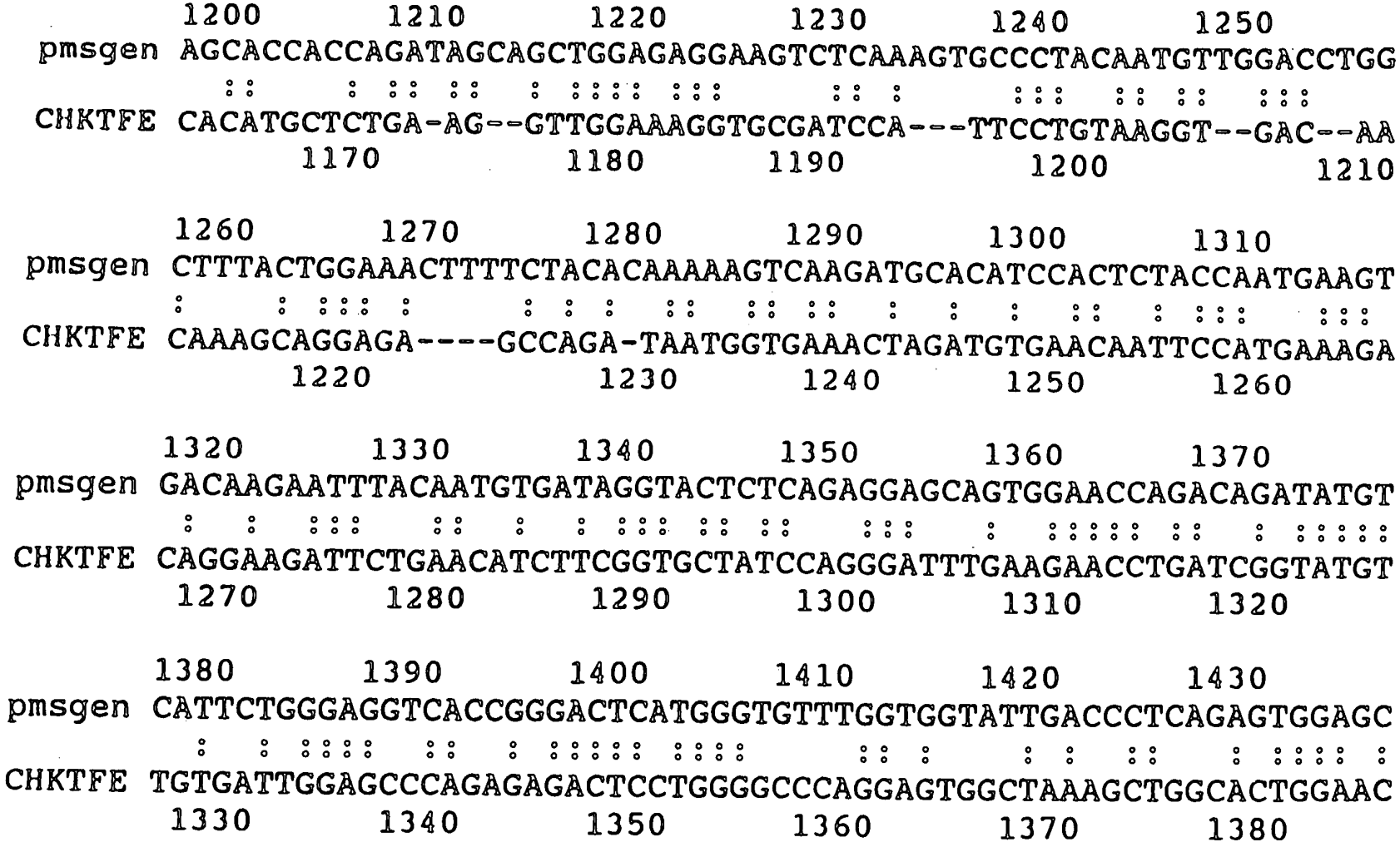
```
☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆
☆ PREDICTION OF ANTIGENIC DETERMINANTS ☆
☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆☆

Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

The method used is that of Hopp and Woods.
The averaging group length is: 6 amino acids.
-> This is the value recommended by the authors <-

-----------------------------------

The three highest points of hydrophilicity are:

( 1)  Ah= 1.62 : From   63 to   68 : Asp-Glu-Leu-Lys-Ala-Glu
( 2)  Ah= 1.57 : From  132 to  137 : Asn-Glu-Asp-Gly-Asn-Glu
( 3)  Ah= 1.55 : From  482 to  487 : Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100%
of the cases assigned to a known antigenic group. The second and third points
gave a proportion of 33% of incorrect predictions.
```


Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-1

```
The best scores are:                                          initn  init1   opt
CHKTFER   G.gallus mRNA for transferrin receptor               203    120    321
RATTRFR   Rat transferrin receptor mRNA, 3′ end.               164    164    311
HUMTFRR   Human transferrin receptor mRNA, complete cd         145    145    266


CHKTFER   G.gallus mRNA for transferrin receptor               203   120   321
  51.9% identity in 717 nt overlap

       1020       1030       1040       1050       1060       1070
pmsgen TGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTA
                                          :::  : ::::::::::  :::: ::::::: :
CHKTFE TACACTTATCCCATTCGGACATGCCCACCTTGGAACTGGAGACCCTTACACCCCAGGCTT
           990       1000       1010       1020       1030       1040

       1080       1090       1100       1110       1120       1130
pmsgen CCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTAT
       :::  :     :  :  :  :   :  :  :   :  ::  ::  ::  ::  ::    ::
CHKTFE CCCTTCGTTCAACCACACCCA---GTTTCCACCAGTTGAATCTTCAGGACTACCCCACAT
          1050       1060          1070       1080       1090       1100

       1140       1150       1160       1170       1180       1190
pmsgen TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTC
       : :::::::  : ::       :  ::  :::   : :::  :     :::::::: :::
CHKTFE TGCTGTTCAGACCATCTCTAGCAGTGCAGCAGCCAGGCTGTTCAGCAAAATGGATGGAGA
             1110       1120       1130       1140       1150       1160
```

FIG. 16-2



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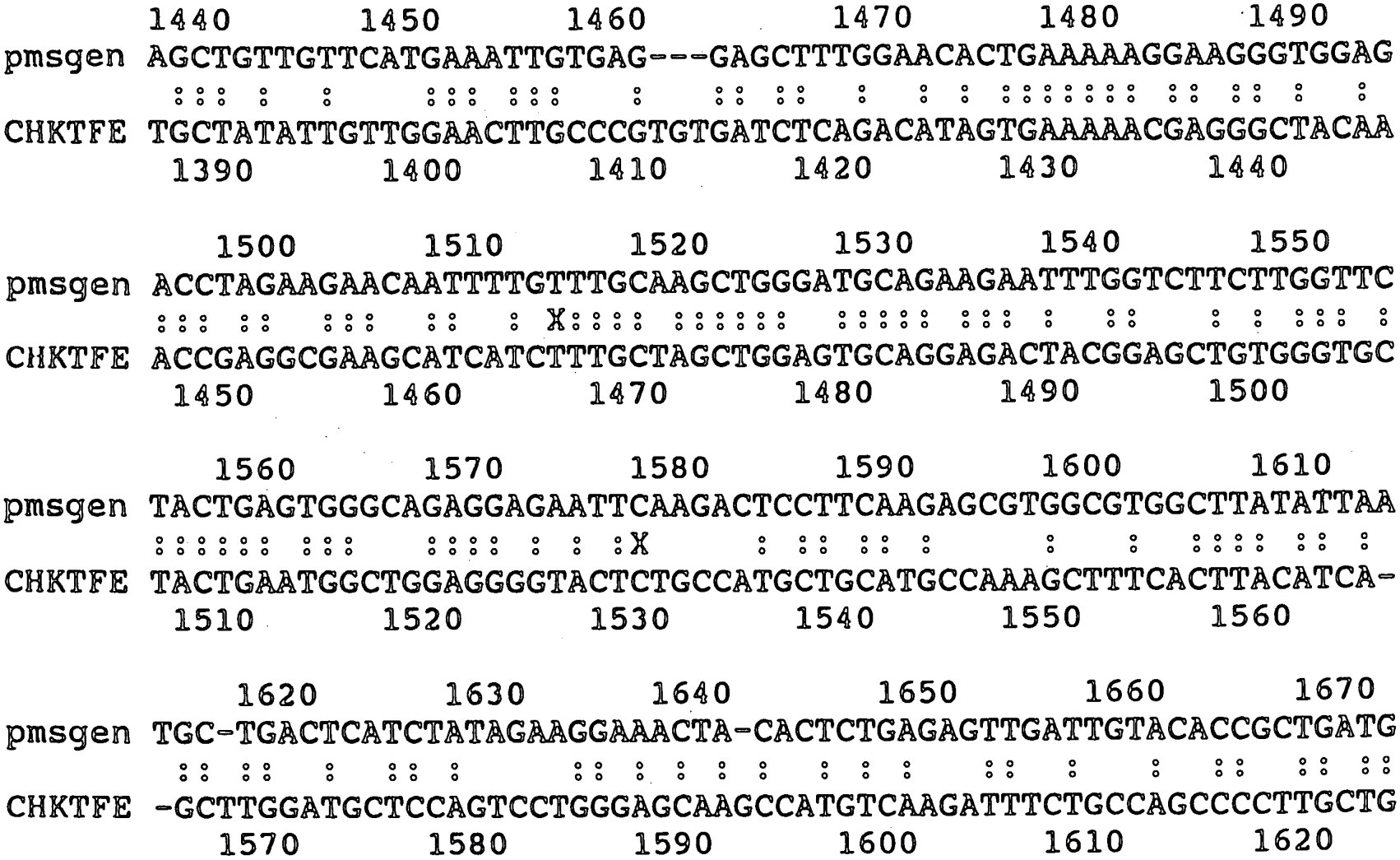
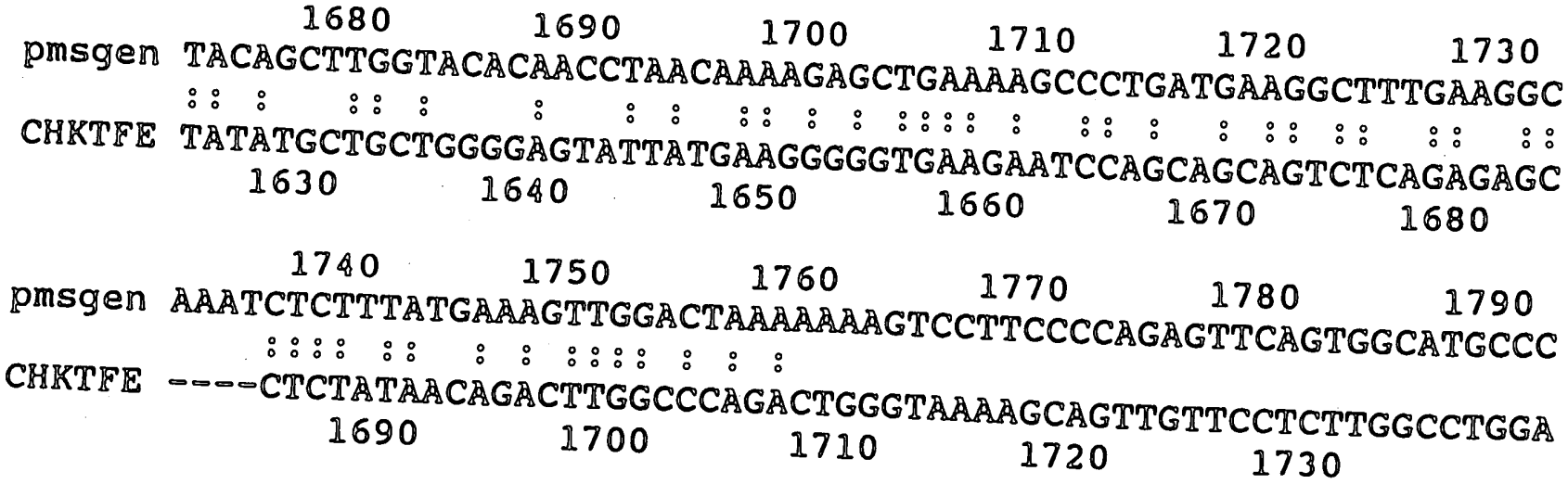
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-3



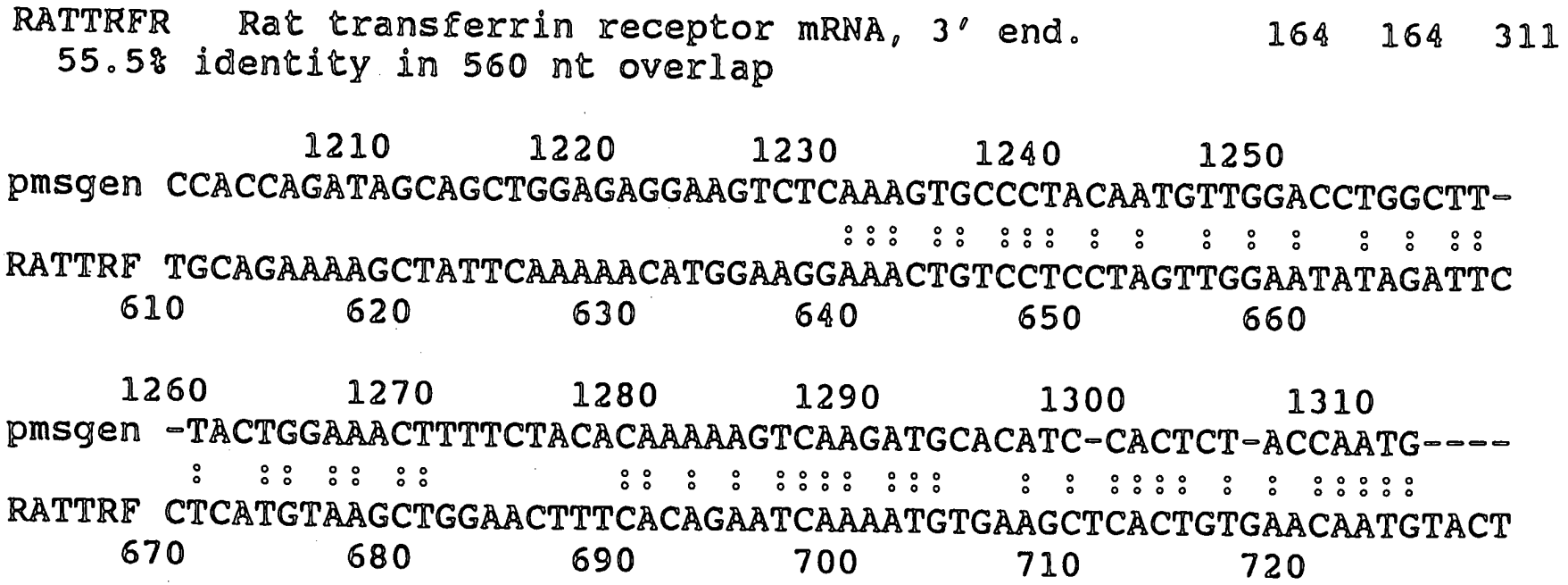
Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-4



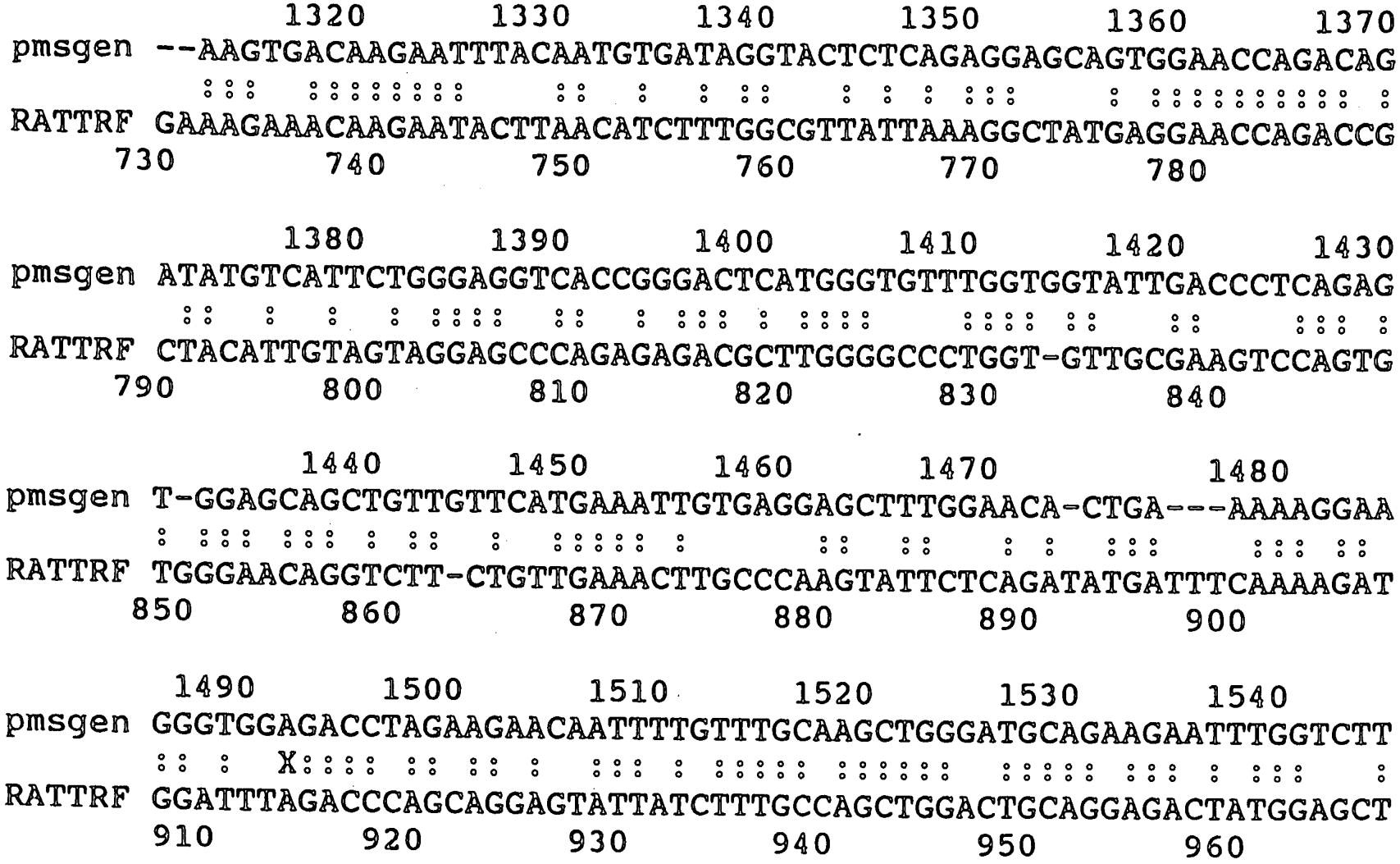
Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-5



Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-6



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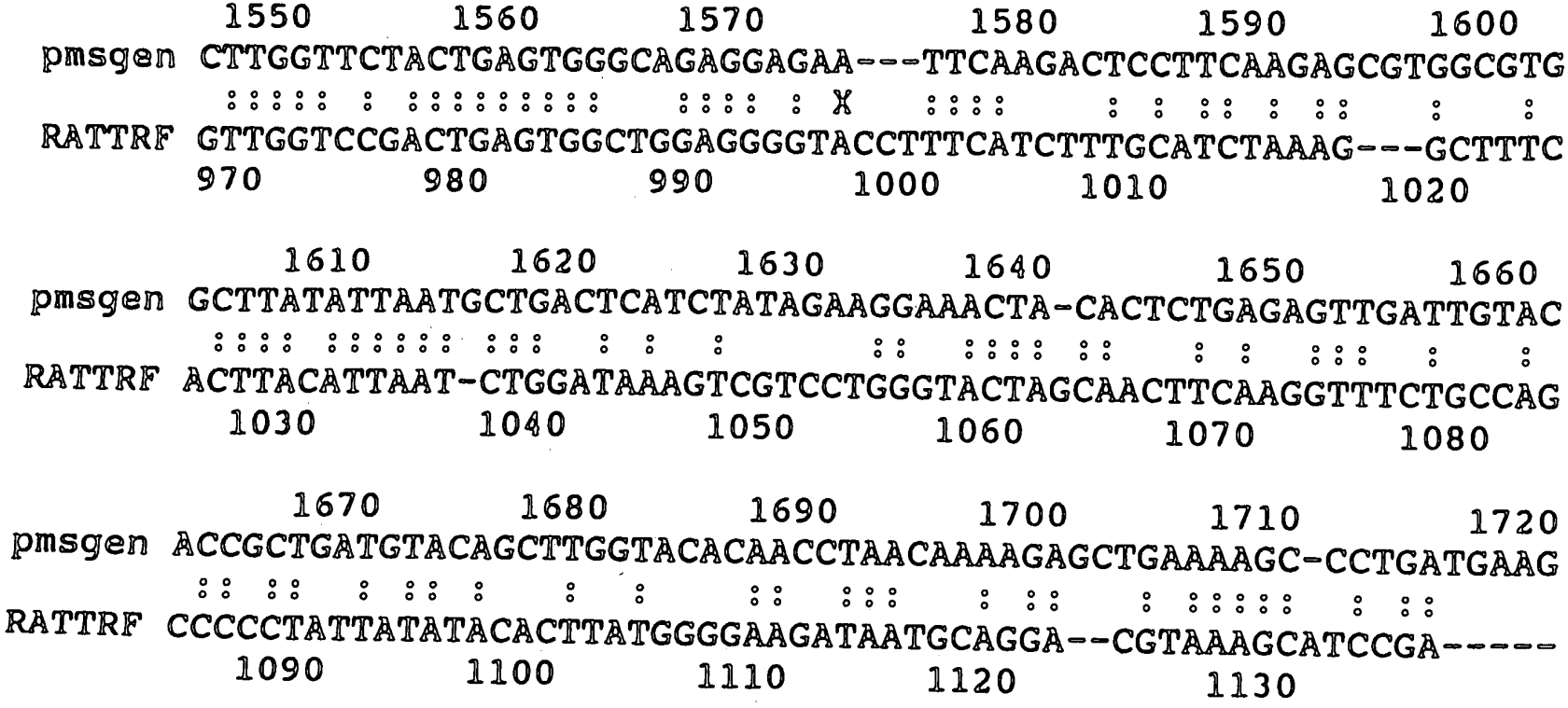
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-7



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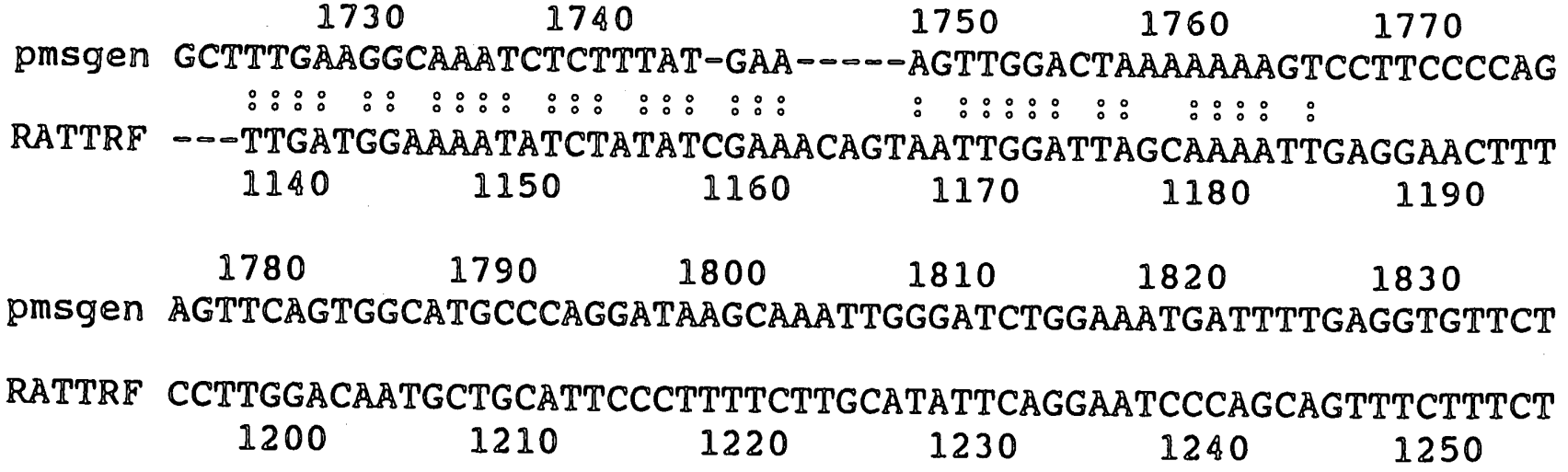
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-8



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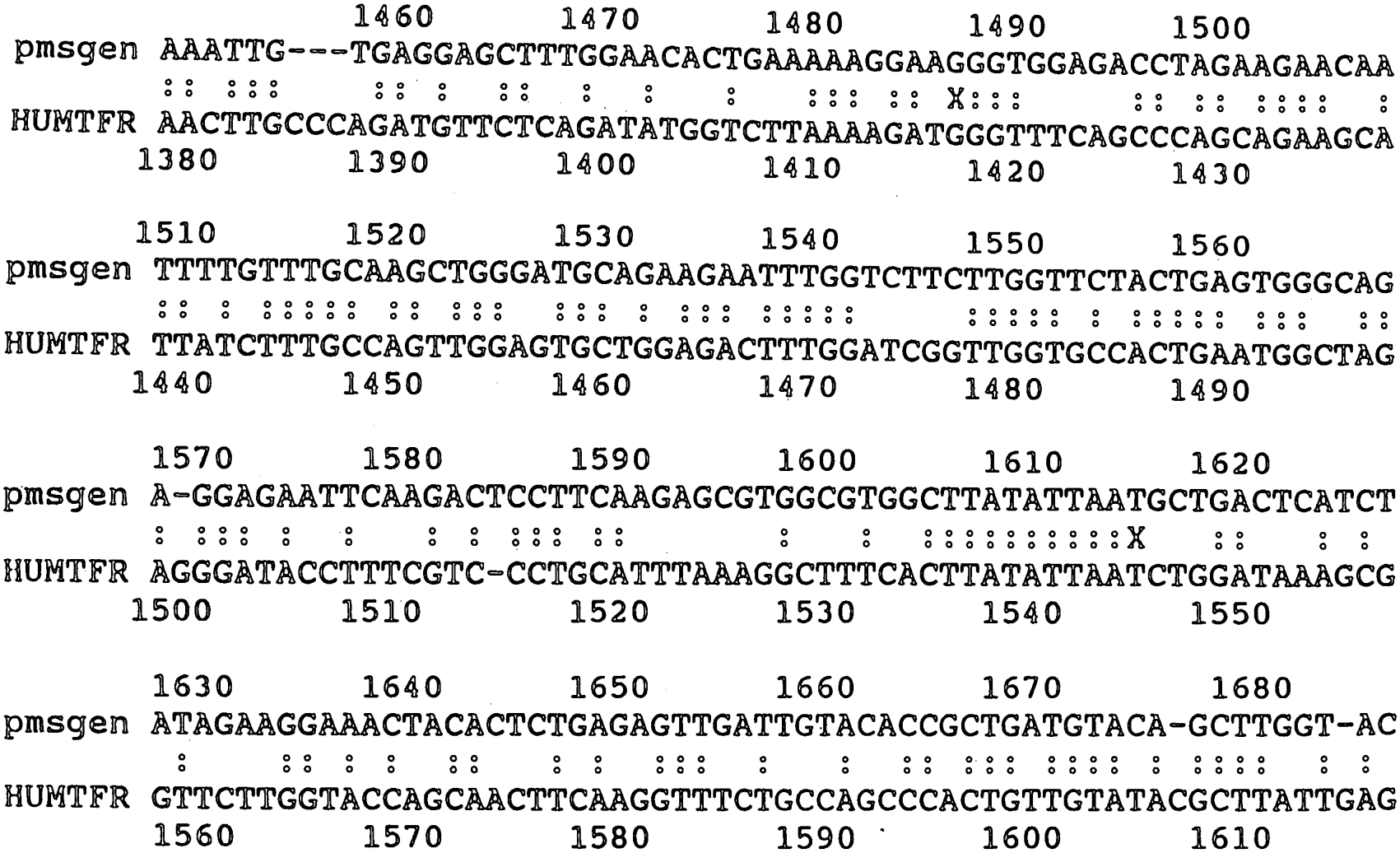
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-9

```
HUMTFRR   Human transferrin receptor mRNA, complete cd  145  145  266
  54.3% identity in 464 nt overlap

              1230       1240       1250       1260       1270
pmsgen AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC
                                                :  :  :  :: ::: :: :  :  :  :  : :
HUMTFR TATGGAAGGAGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTAGGATGGTAACCTC
     1140       1150       1160       1170       1180       1190

    1280       1290       1300       1310                  1320       1330
pmsgen AAAAAGTCAAGATGCACATC-CACTCT-ACCAATG------AAGTGACAAGAATTTACAA
        :  :::::  :  :::    :  :  :::::  :  :  ::::::       ::: ::  ::  ::::::    ::
HUMTFR AGAAAGCAAGAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAAATTCTTAA
     1200       1210       1220       1230       1240       1250

             1340       1350       1360       1370       1380       1390
pmsgen TGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCA
          :   :  ::    :  :  :  :::    :: ::::::::      :::::  :  :  ::  :  ::
HUMTFR CATCTTTGGAGTTATTAAAGGCTTTGTAGAACCAGATCACTATGTTGTAGTTGGGGCCCA
     1260       1270       1280       1290       1300       1310

             1400       1410       1420       1430       1440       1450
pmsgen CCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATG
          :  ::   ::::::     ::: :  :     :   :  :  :  ::  ::   ::::::  :   :
HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA
     1320       1330       1340       1350       1360       1370
```

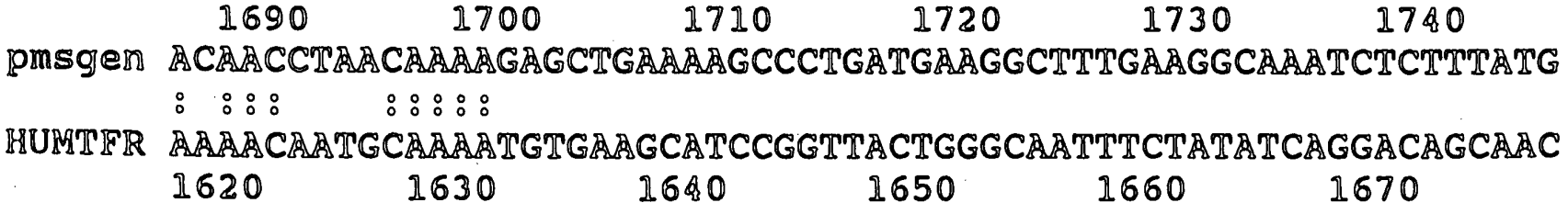

Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-10



Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIG. 16-11



Title: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
Applicants: Ron S. Israeli, et al.
U.S. Serial No. 08/466,381
Filed: June 6, 1995

FIGURE 17A

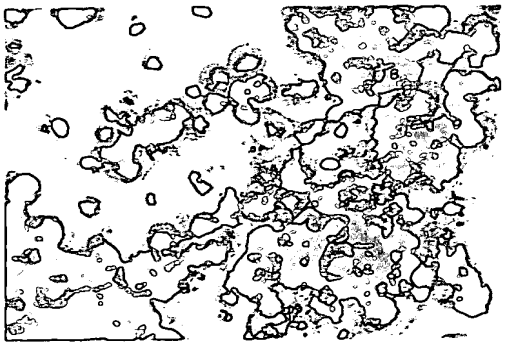


FIGURE 17B

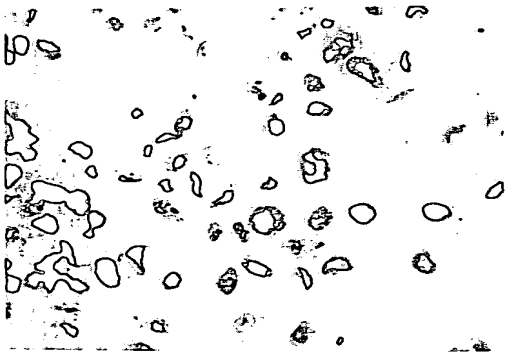


FIGURE 17C

FIGURE 18

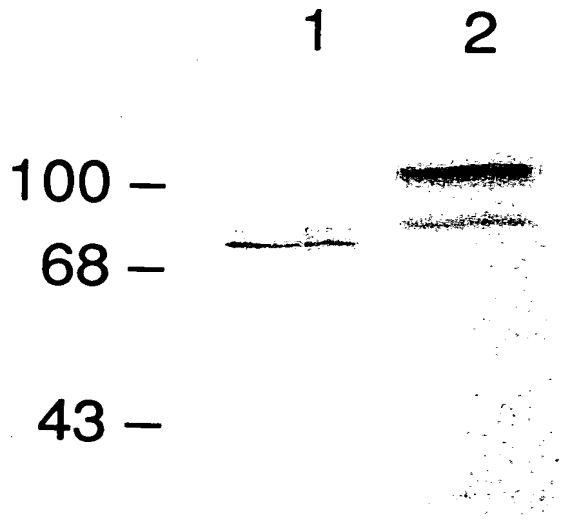
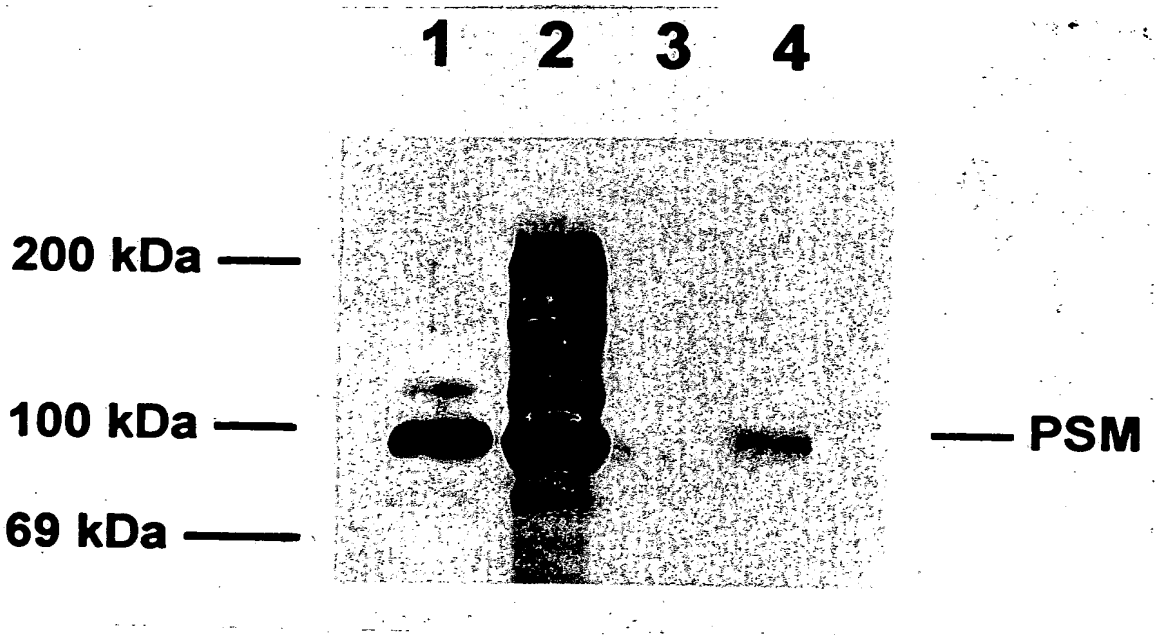


FIGURE 19



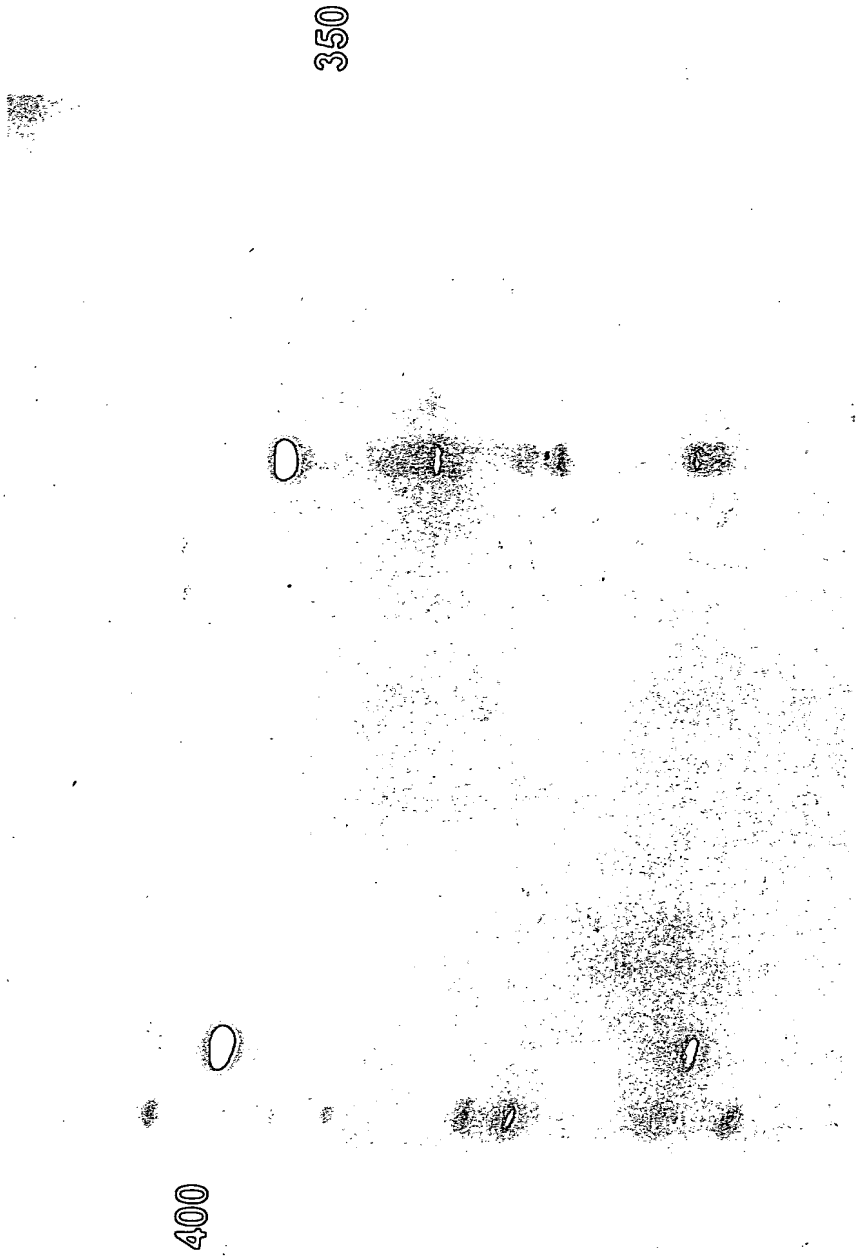


FIGURE 20

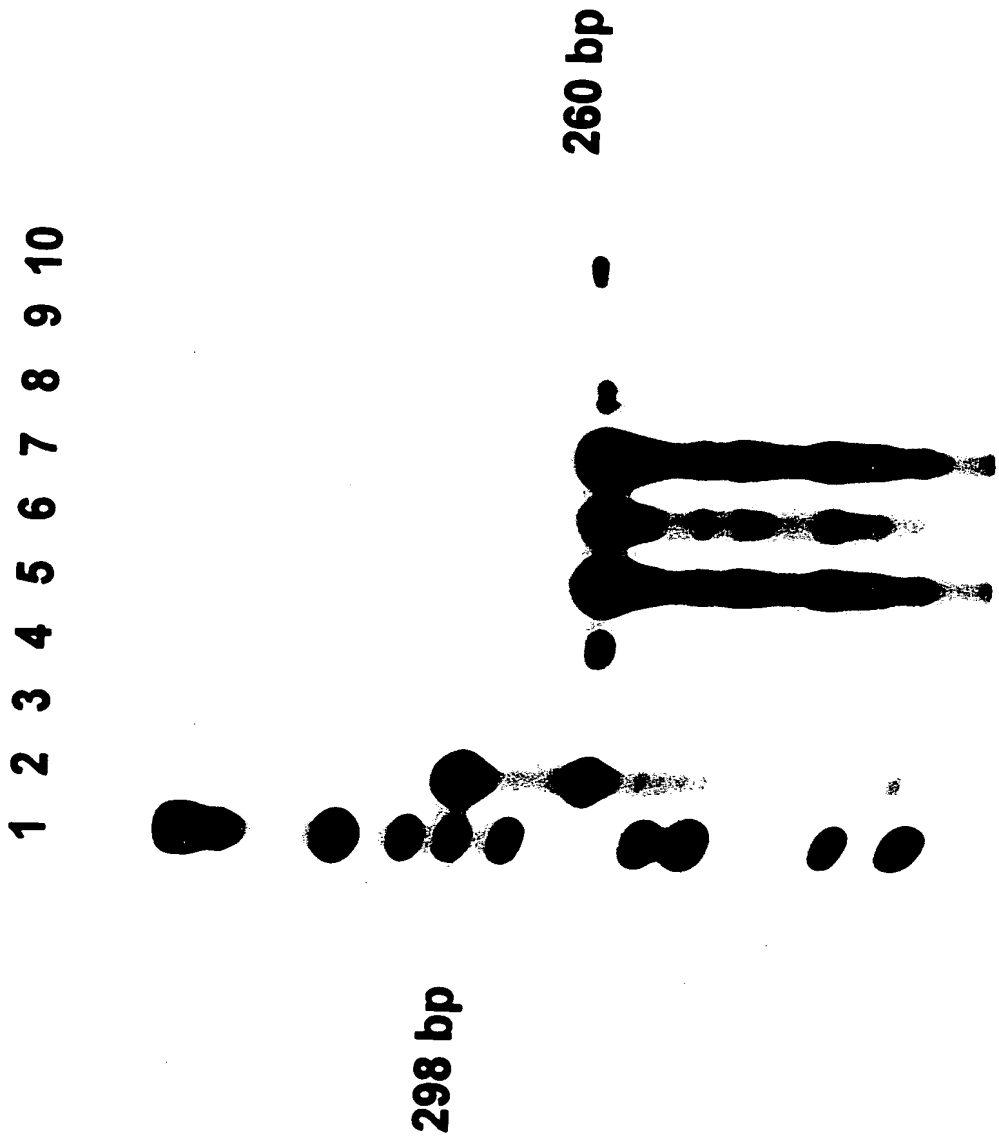


FIGURE 21

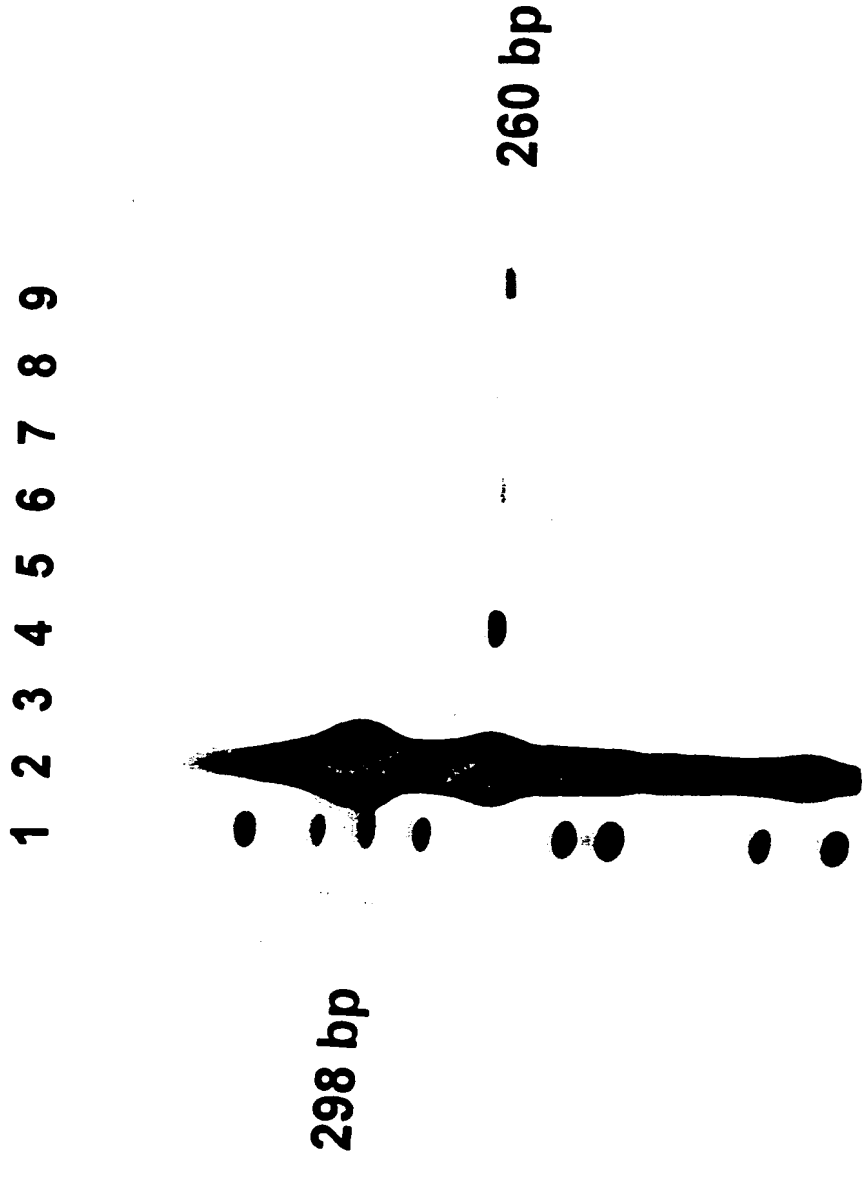


FIGURE 22

FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	–	–
A9(11) (A9+HUM. 11)	YES	NO	–	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	–	–
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	–	–
R1564 (RAT MAMMARY)	NO	YES	–	–
R1564-11-c14	YES	YES	–	+
R1564-11-c15	YES	YES	–	REPEAT
R1564-11-c16	YES	YES	–	ND
R1564-11-c12	YES	YES	ND	+

FIGURE 24A

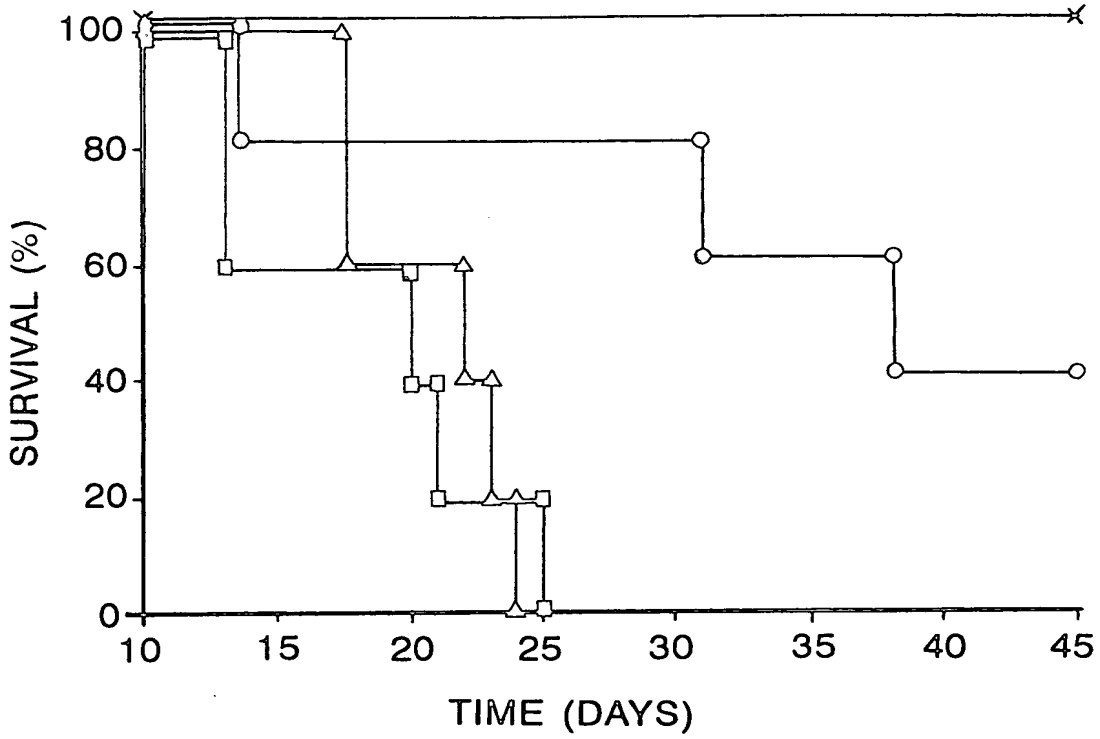


FIGURE 24B

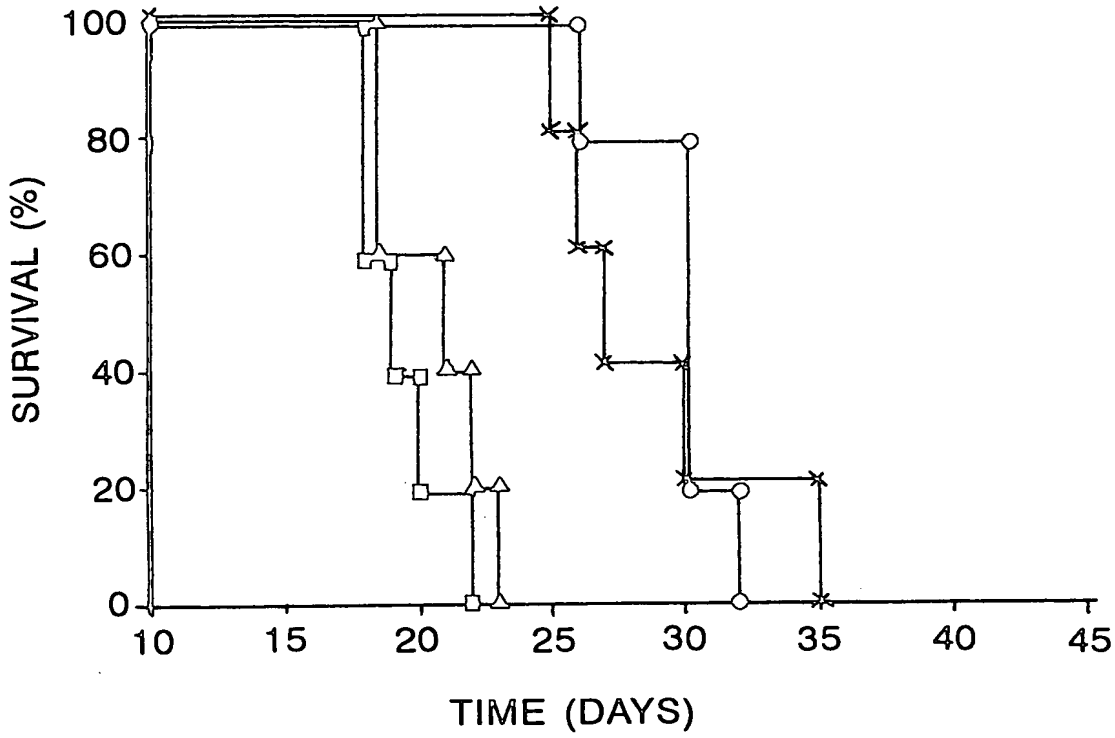


FIGURE 25A

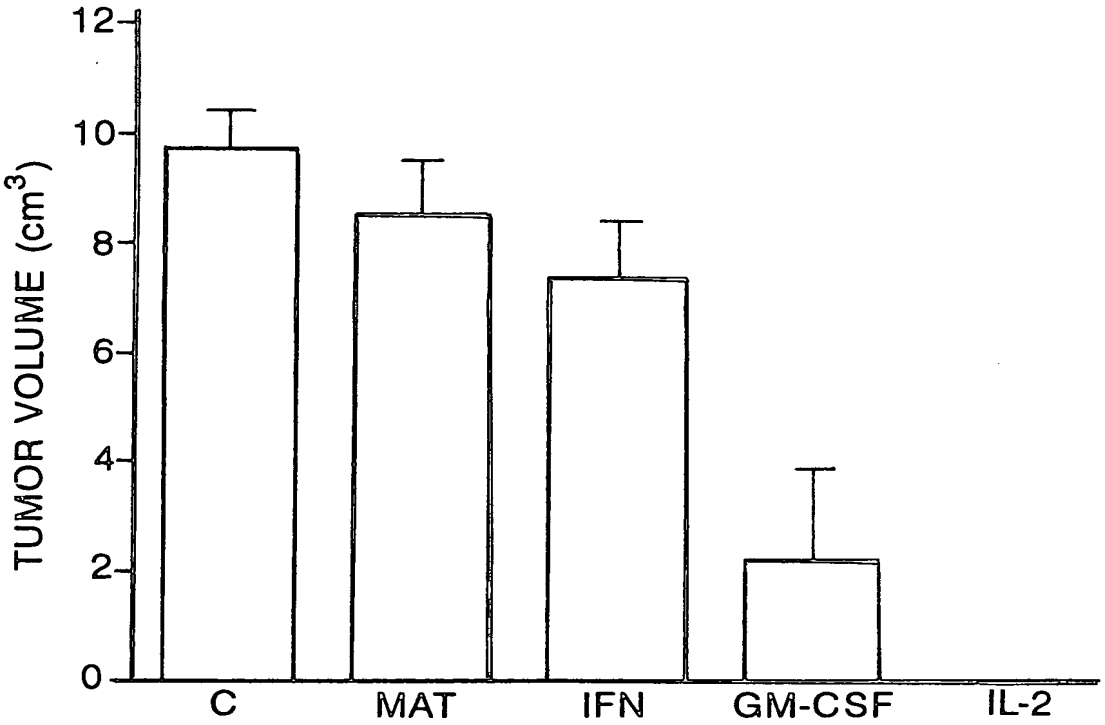
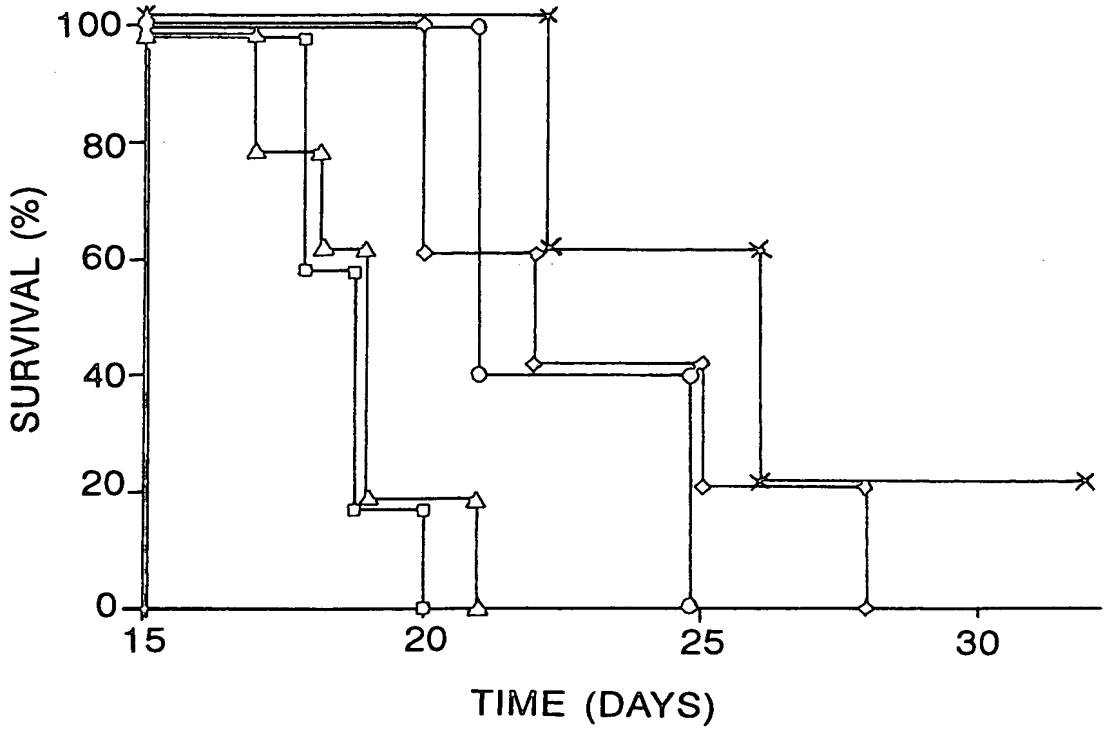


FIGURE 25B



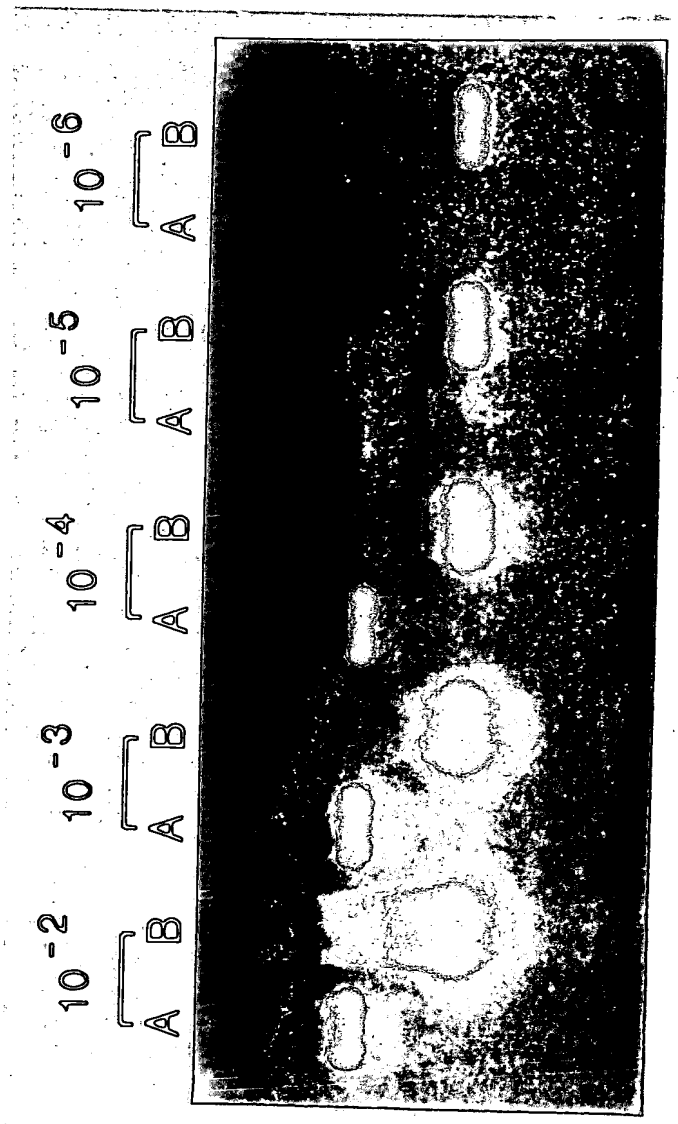
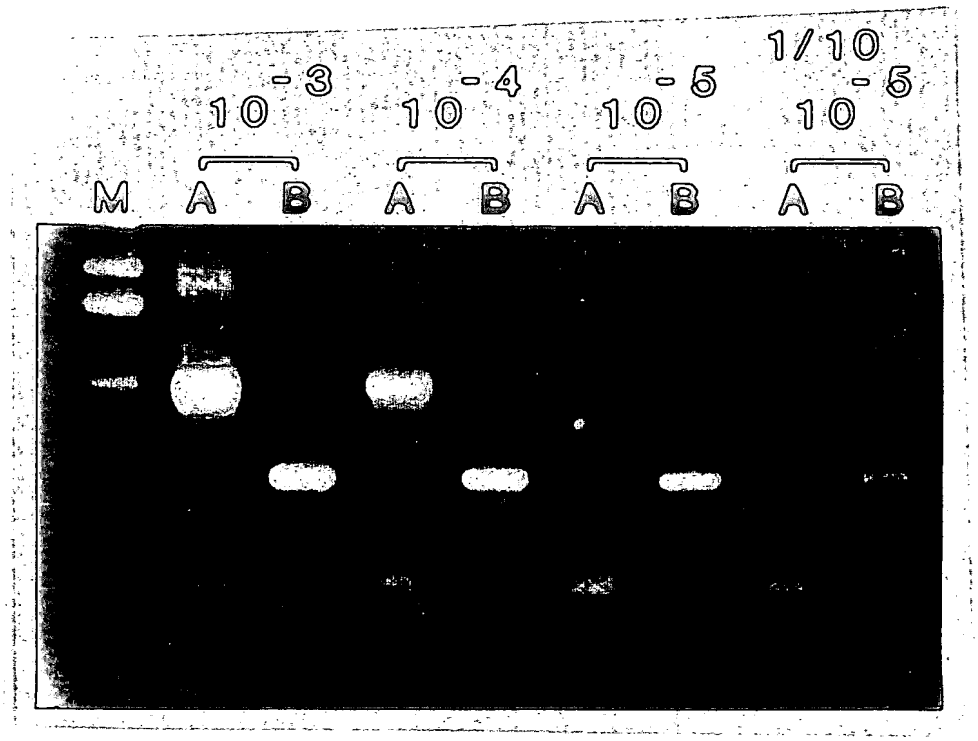


FIGURE 26

FIGURE 27



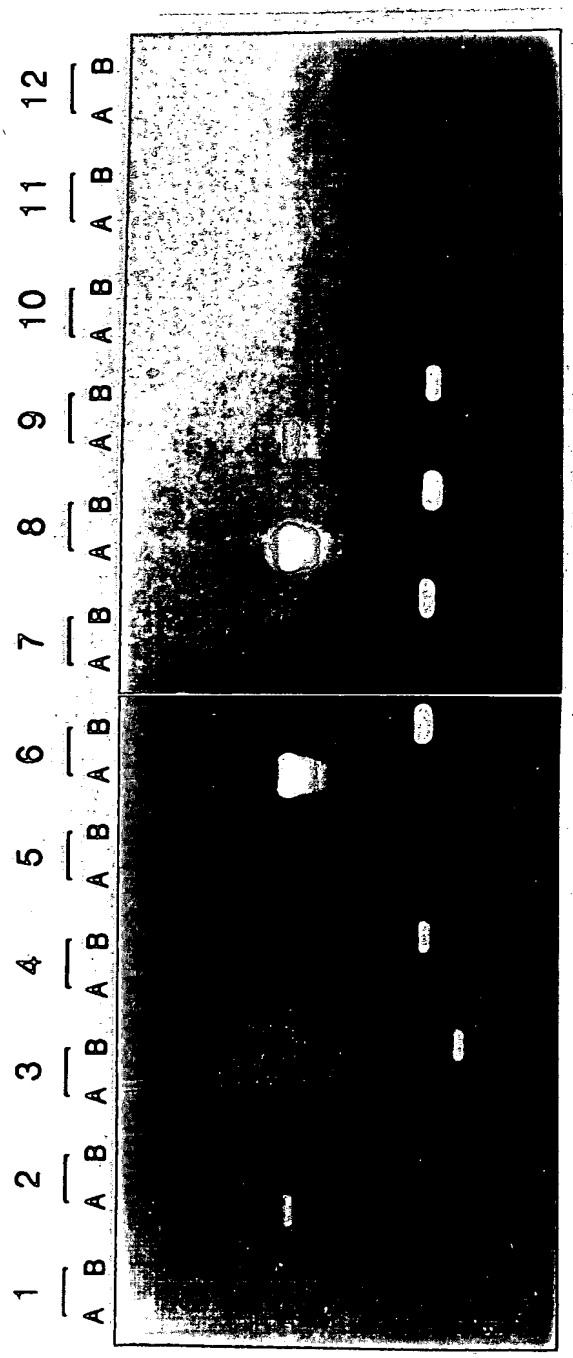


FIGURE 28

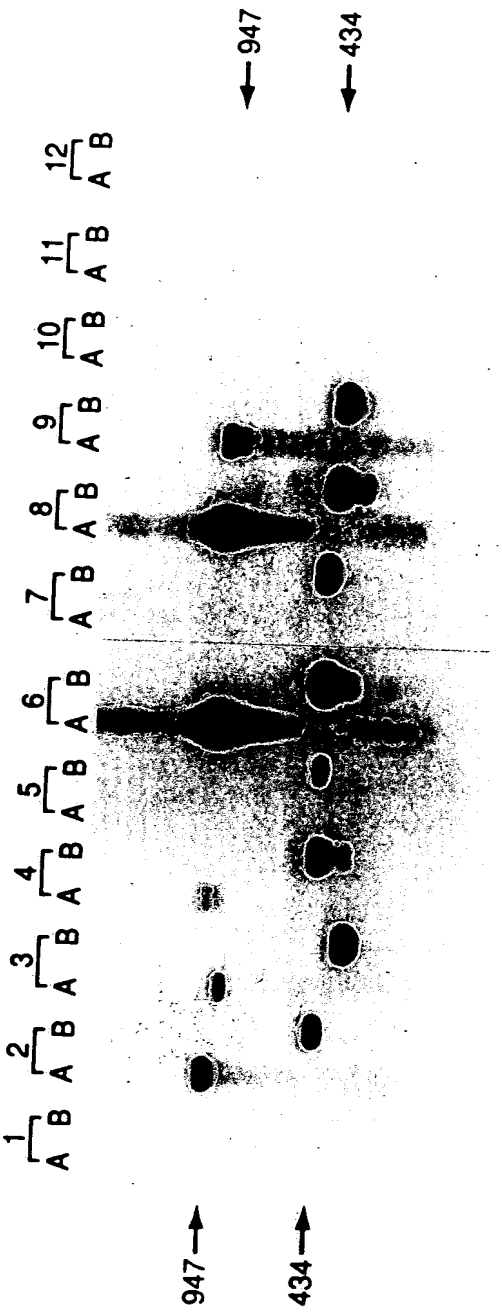

947
434
12 A B
11 A B
10 A B
9 A B
8 A B
7 A B
6 A B
5 A B
4 A B
3 A B
2 A B
1 A B
947
434

FIGURE 29

FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	–	+
2	T2NoMo	RRP 7/93	6.1	–	–	+
3	T2CNoMo	PLND 5/93	4.5	0.1	–	+
4	T2BNoMo	RRP 3/92	NMA	0.4	–	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	–	+
6	Recur T3	I-125 1986	54.7	1.4	–	+
7	T3ANoMo	RRP 10/92	NMA	0.3	–	+
8	T3NxMo	XRT 1987	7.5	0.1	–	–
9	T3NxMo	Proscar + Flutamide	35.4	0.7	–	–
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	–	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	–	–
14	D1	PLND 1989 XRT 1989	1.6	0.4	–	–
15	D1	Proscar + Flutamide	20.8	0.5	–	–
16	T2CNoMo	RRP 4/92	0.1	0.3	–	–